

FIGURE 1A

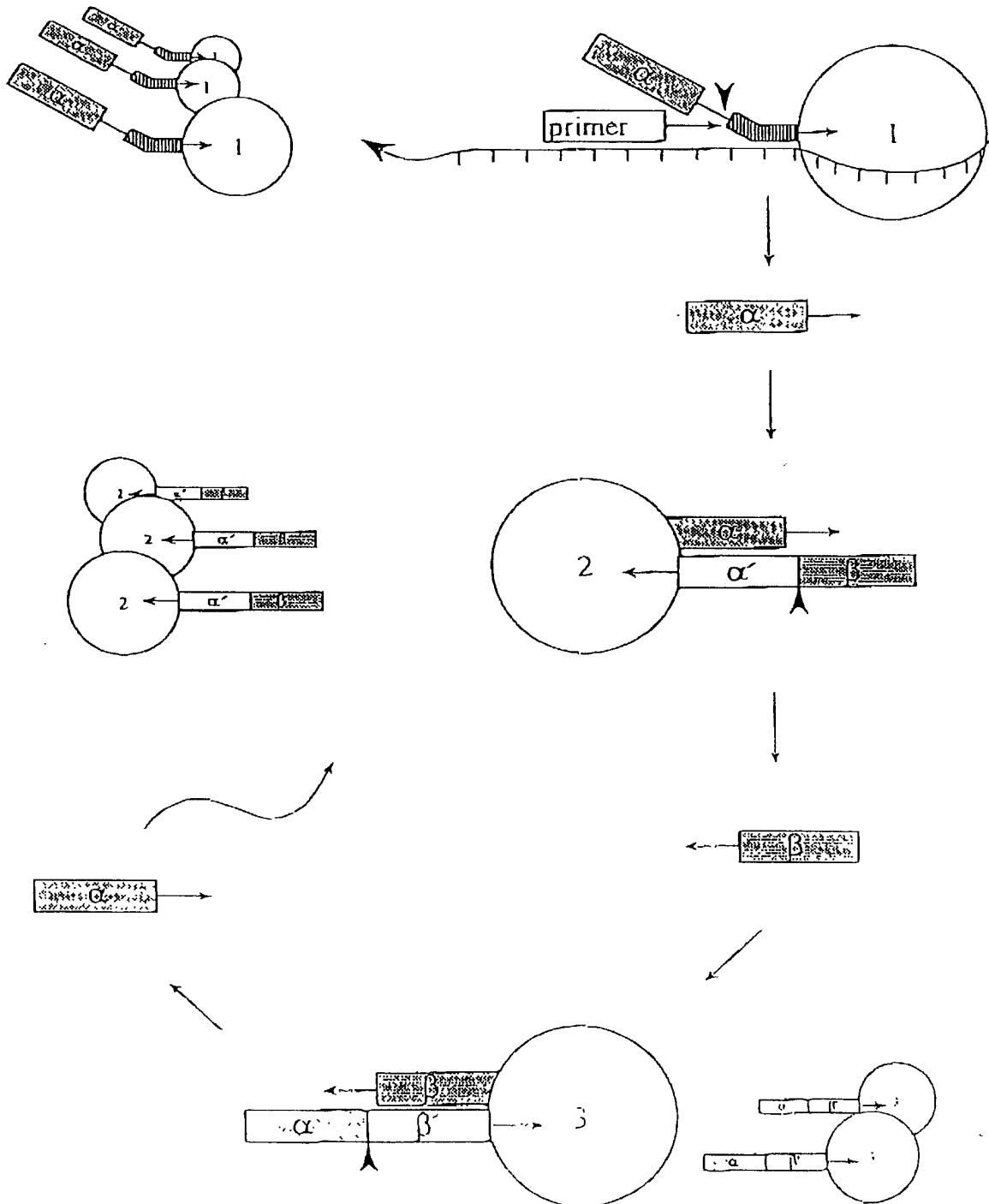
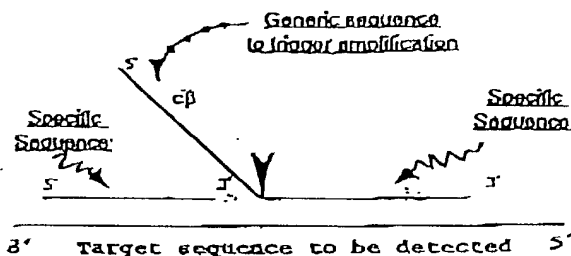


FIGURE 1B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION

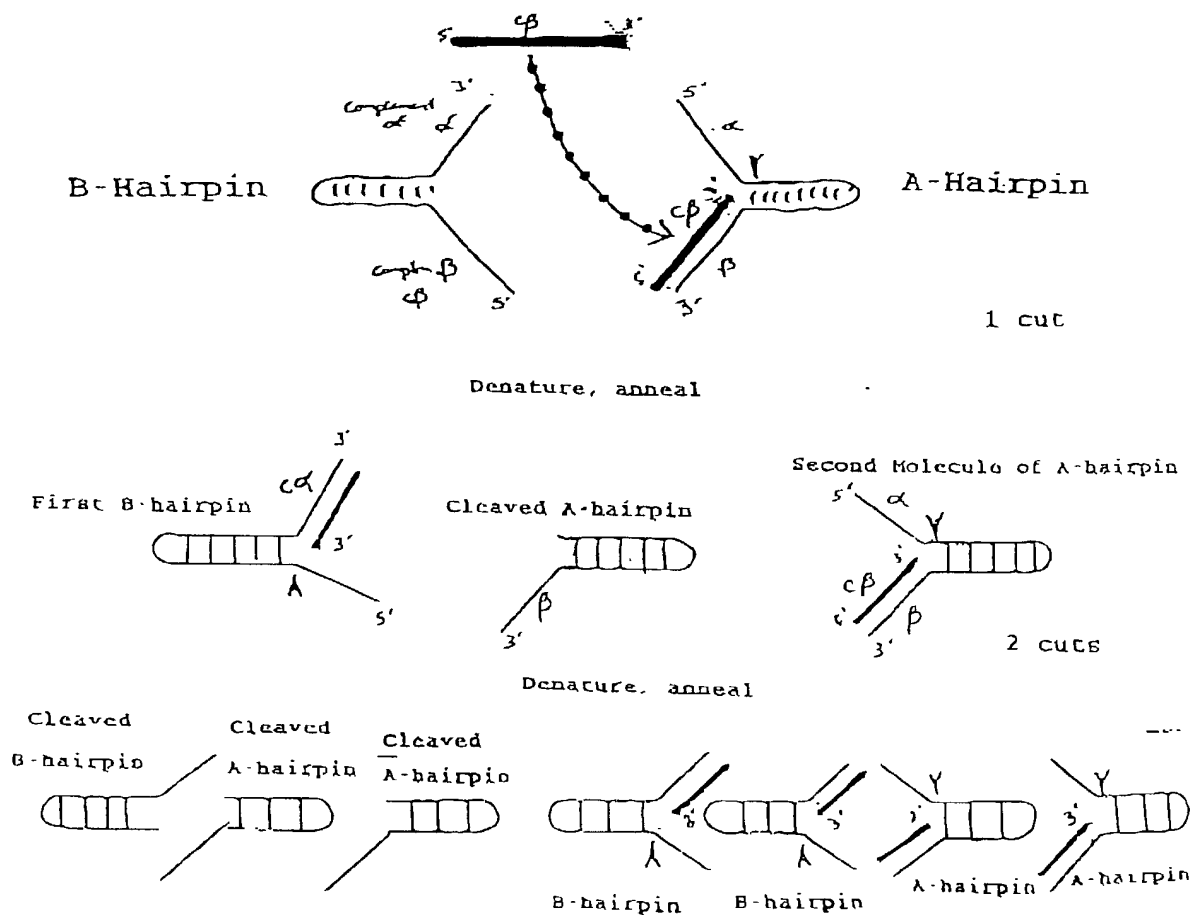


FIGURE 2

MAJORITY (SEQ ID NO:7)	A T C X X G G C C A T C C T T C G G C T G T T T G A C C C C A A A G C C C C C C C T C C T C C T G G T G A C C G G C C A G C C T G C C C T	70
DNAPTAD (SEQ ID NO:1)	... A C . . . G G C G	67
DNAPTFL (SEQ ID NO:2)	70
DNAPTTH (SEQ ID NO:3)	... G A G A .	
MAJORITY	A C C G C A G C T T C T T C C C C C T G A A C C C C C T C A C C A C C A C C C C G G C C A A C C C C T C C A C C C C G G T C T A C C C C C T T	140
DNAPTAD	137
DNAPTFL	140
DNAPTTH	
MAJORITY	C C C C A G A G C C T C C T C A A G C C C C T G A A G C C A G C A C C C C C C A C X X C C C C C G T C X T C G T G T C T T T G A C C C C A A G	207
DNAPTAD	204
DNAPTFL	210
DNAPTTH	
MAJORITY	G C C C C C C T C C T T C C C C C A C C A C C C C T A C G A G C C C T A C A A G C A G C C T T T C	277
DNAPTAD	274
DNAPTFL	280
DNAPTTH	
MAJORITY	C C C C C C A C C T C C C C C T C A T C A A C C A G C T C C T C G A C C T C C T G C C C C C C T T C C C C C C C C C T C C A C C T C C C C C C C C T A	347
DNAPTAD	344
DNAPTFL	350
DNAPTTH	

3

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	CCAGCCCGCAGCAGCTXCTGCGGACCGCTGGCCAAAGCGCGGCAAAAGCAGGGGTACGAGGTCGGGATCCCTC	
DNAPTAA (SEQ ID NO:1)C.....G.....C.....C.....	417
DNAPTFL (SEQ ID NO:2)G.....CG.....	414
DNAPTH (SEQ ID NO:3)T.....C.....	420
MAJORITY	ACCGCCCGCAGCAGCTGACGAGGTCCTTTCCGACCGGATCGCGGTCCTCCAGCCCGGACGGGTACCTCA	
DNAPTAA (SEQ ID NO:1)AAA.....T.....CA.....	487
DNAPTFL (SEQ ID NO:2)T.....G.....G.....A.....T.....G.....	484
DNAPTH (SEQ ID NO:3)A.....G.....G.....G.....CC.....	490
MAJORITY	TCAGCCCGCGCTGCTTCCGACAGCTACCGGCTCAGCGCGGCGGACCACTGGGTGGACTACCGCGCGCTCCG	
DNAPTAA (SEQ ID NO:1)C.....A.....A.....C.....C.....CC.....A.....	557
DNAPTFL (SEQ ID NO:2)AC.....AC.....C.....C.....C.....C.....	554
DNAPTH (SEQ ID NO:3)A.....A.....C.....C.....C.....T.....C.....T.....	560
MAJORITY	CGCGGACCCCTCCGACCAAGCTCCCGCGGCTCAAGCGGATCGCGGACCAAGCGGCGGCGGCTCCCTCXAG	
DNAPTAA (SEQ ID NO:1)GAG.....T.....T.....G.....GAG.....T.....CG.....	627
DNAPTFL (SEQ ID NO:2)G.....I.....A.....G.....A.....A.....A.....A.....CGG.....	624
DNAPTH (SEQ ID NO:3)G.....I.....A.....G.....T.....T.....A.....	630
MAJORITY	GAGTCGGCGCAGCGCTGGAAAGCTGCTCAAGAACCTGCGACCGGCTCAAGCGCGGCGGCGGCTCGTCCCGGACAGAGA	
DNAPTAA (SEQ ID NO:1)CG.....CG.....C.....C.....A.....	694
DNAPTFL (SEQ ID NO:2)I.....C.....C.....A.....T.....T.....C.....C.....	691
DNAPTH (SEQ ID NO:3)A.....A.....A.....A.....A.....A.....A.....A.....C.....	700

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1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FIGURE 2 (cont'd)

[illegible]

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	CGAGATCCCGCGCGCTCGAGCAAGAGGTCCTCCCGCTCCCGCGCGCGCGCTTCAACCTCAACTCCCGCGGAC	1464
ONAPTAO (SEQ ID NO:1)CG.....CG.....	1461
ONAPTR (SEQ ID NO:2)G.....AC.....G.....T.....G.....	1461
ONAPTH (SEQ ID NO:3)	1461
MAJORITY	CAGCICGAAAGGCTCCTCTTTCAGCAGGCTXCGGCTTCCCGCGCTCCCGCAAGAGCGGCAAGACXCGGCAAGC	1534
ONAPTAOG.....A.....G.....G.....G.....G.....A.....	1531
ONAPTRGC.....G.....G.....G.....T.....T.....G.....G.....A.....	1540
ONAPTHTA.....T.....G.....G.....A.....	1540
MAJORITY	GCICGACACCGCGCGCGCTCGTCGAGCGGCTXCGXAGCGCGCGCGCGCTCGTCGAGAGATCCICGACGTA	1604
ONAPTAOG.....C.....C.....C.....C.....C.....C.....C.....C.....	1601
ONAPTRT.....G.....G.....G.....G.....G.....G.....G.....G.....	1610
ONAPTHG.....A.....G.....A.....G.....A.....G.....A.....G.....	1610
MAJORITY	CGCGGAGGTCACCAAGCICAAAGAACACACCTACATXGACCGCGCTCCCGCGCGCTCGTCGAGCGCGCGCGCG	1680
ONAPTAOG.....G.....T.....T.....G.....A.....A.....A.....A.....	1680
ONAPTRA.....A.....A.....A.....A.....A.....A.....A.....	1680
ONAPTHG.....G.....G.....G.....G.....G.....G.....G.....	1680
MAJORITY	CCCCCAGACACCGCGCTCAACCAACACCGCGCGCGCGCGCGCGCGCTAGTAGCTCGGACCGCGCGCGCG	1744
ONAPTAOA.....A.....A.....A.....A.....A.....A.....A.....	1741
ONAPTRG.....G.....G.....G.....G.....G.....G.....G.....	1750
ONAPTHG.....G.....G.....G.....G.....G.....G.....G.....	1750

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	ACAACATCCCGGTCGCCACCCXCTGCCCCAGAGCAATCCCGCGGGCTTCCTGCCCGAGGCGXTCGGT	
DNAPTAD (SEQ ID NO:1)G..T..G.....A..C.....C...C..	1814
DNAPTR (SEQ ID NO:2)G.....T.....C.C.....A.....C.....C.....	1811
DNAPTH (SEQ ID NO:3)GT.....C.....C.....T.....C.....C.....	182
MAJORITY	CTTGGTGGCCCTCCACIATAGCCACATAGAGGTCGGGGTCTCTGCCGGAACCTCTCGGGGAGGAGACCGTC	
DNAPTAD	A.....T.....A.....G.....C.....	1884
DNAPTR	.C.....T.....C.....T.....T.....C.....A.....	1881
DNAPTHT.....C.....C.....C.....A.....	1890
MAJORITY	ATCCGGGCTCTCCAGAGCGGAGGACATCCAGAGCCAGAGCGGCGAGCTGGATCTTCGGCGTCCCGCCGG	
DNAPTADG.....GG.....G.....C...	1954
DNAPTRT.....A.....A.....T.....C...	1951
DNAPTHA.....A.....A.....	1960
MAJORITY	ACGGCCCTCCACCGCCCTGATCGCGCGGCGGCGGCAAGACCATCAACTTCGGCGTCCCTCTAGCGGCACTCCGG	
DNAPTADA..GG..A.....T.....GG.G.....C.....G...	201
DNAPTRA..GG..A.....T.....GG.G.....C.....G...	2021
DNAPTHA..GG..A.....T.....GG.G.....C.....G...	2030
MAJORITY	CCACCGCCCTCTCCAGGAGCTTCCCATCGCGCTACGAGGCGGCTCGCGCTTCATTCAGCGGCTACCTCCAG	
DNAPTADA.....T.....CCA.....T...	2094
DNAPTRGG.....T.....T.....T.....A.....	2097
DNAPTHTA.G.....T.....T.....A.....A.....	2100

FIGURE 2 (cont'd)

[illegible]

FIGURE 3

MAJORITY (SEQ ID NO:6)	HXAHLPLFEPKGRVLLVGGHLLAYRTFFALKOLTTSRCEPVQAVYGFAKSLLKALKEDG·OAVXVVVFOAX	29
1A0 PRO (SEQ ID NO:4)	AC.....H.....I.....	70
TR PRO (SEQ ID NO:5)V.V.....YK..F.....	
TH PRO (SEQ ID NO:6)	E.....	
MAJORITY	APSFRAEAYEAYKACRAPTPEOFPAOLALIKELVDLLGLXALEVPGYEADOVLATLAKXAÆKEGYEVAIL	139
1A0 PRO	GC.....A.....S.....	138
TR PROU.....F.....R.....	140
TH PROFI.....	
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVOYRALXODPSDNLPOVKGIGENTAXKLLX	209
1A0 PRO	K.....H.....D..A.....I..E.....R...E	208
TR PROE..I.....Y.....A.....I.....OR..A	210
TH PROV..V.....H.....E.....F..V.....L...K	
MAJORITY	EWGSLNLLKNLORVKP·XXREKIXAHMEOLXLSXXLSXVATOLPLEVDFAXRAEPDREGLRAFLERLEF	278
1A0 PRO	A.....L...A...L...D...K...WO..AK.....K.....R.....	277
TR PRO	FOH..O...SL...LO..G..A..A..RK..O..H.....GR..I..NL.....	280
TH PRO	ENV.....K..L...R..LE..R.....L..OO.....	
MAJORITY	GSILHEFGLLEXPKALCEAPWPPPECAFVQFVLSAPEPWAELLALAAARXGRVHRAOXOPLXGLRDLKIV	348
1A0 PRO	S.....K.....D.....G.....PE..YKA.....A	347
TR PRO	C...A.....L..SF.....G..WE..L...O...R.....G..	350
TH PRO	A..AP.....K.....C..D.....A...A..K.....	

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	AGLLAXOLAVLALREGLXPCDDPHL LAYLLOPSNTTPEGVARRYGCWTFEDAGERALLSERLFXNLXX	
TAQ PRO (SEQ ID NO:4)	S.....G.P.....E.....A.....A.....WC	488
TR PRO (SEQ ID NO:5)	I.....F.E.....A.....OT,KE	487
TTX PRO (SEQ ID NO:6)	S.....V.....AH.....HR..LK 420	490
MAJORITY	RIEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEI RRLSEEVRACHPFNLNSAO	
TAQ PRO	R...R...A...A.....R.....A.....A.....	488
TR PRO	E.....R.....EA.V.O.....	487
TTX PRO	K.....H.....L.....	490
MAJORITY	OLERVLFDELGLPAIGKTEKTGXASTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPLVHPRTG	
TAQ PROS.....D.I.....	558
TR PRODR.....A.....K..	557
TTX PRO	A...L...O.....H.....V.....S.....	560
MAJORITY	RLHTRFNOJATATGALSSSDPHLONI PVATPLGORI RRAFVAEEGWXLVALDYSOIELRVLAHLSCDNL	
TAQ PROI.....L.....	628
TR PROV..V.....	627
TTX PROA..A.....	630
MAJORITY	I AVFOECRODHTQTASWMFQVPPPEAVDPLHARA AKTIHFGVLVGMASHALSDLAIPYEEAVAFIERYFO	
TAQ PRO	E.....R.....O.....	698
TR PRO	S..G.....C..S.....	697
TTX PRO	K.....V.....	700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRWIEKTLFEGRRRCYVETLFCRRRYVPDLNAAVKSVREAAERMAFNMPVQOTAAADLWKLAMVXL	760
1A0 PR0 (SEQ ID NO:4)E.....	767
TR PR0 (SEQ ID NO:5)G.....	770
TTX PR0 (SEQ ID NO:6)K.....	
MAJORITY	FPRLEXEMGARMLOVHDELVLLEAPKXRAEXXVAALAKEVMEGVYPLAVPLEVEVQXGEOWLSAKEX	
1A0 PR0E.....	833
TR PR0D.....	831
TTX PR0QA.....	835
R.....	
A.....	
W.....	
O.....	
H.....	
G.....	

FIGURE 4

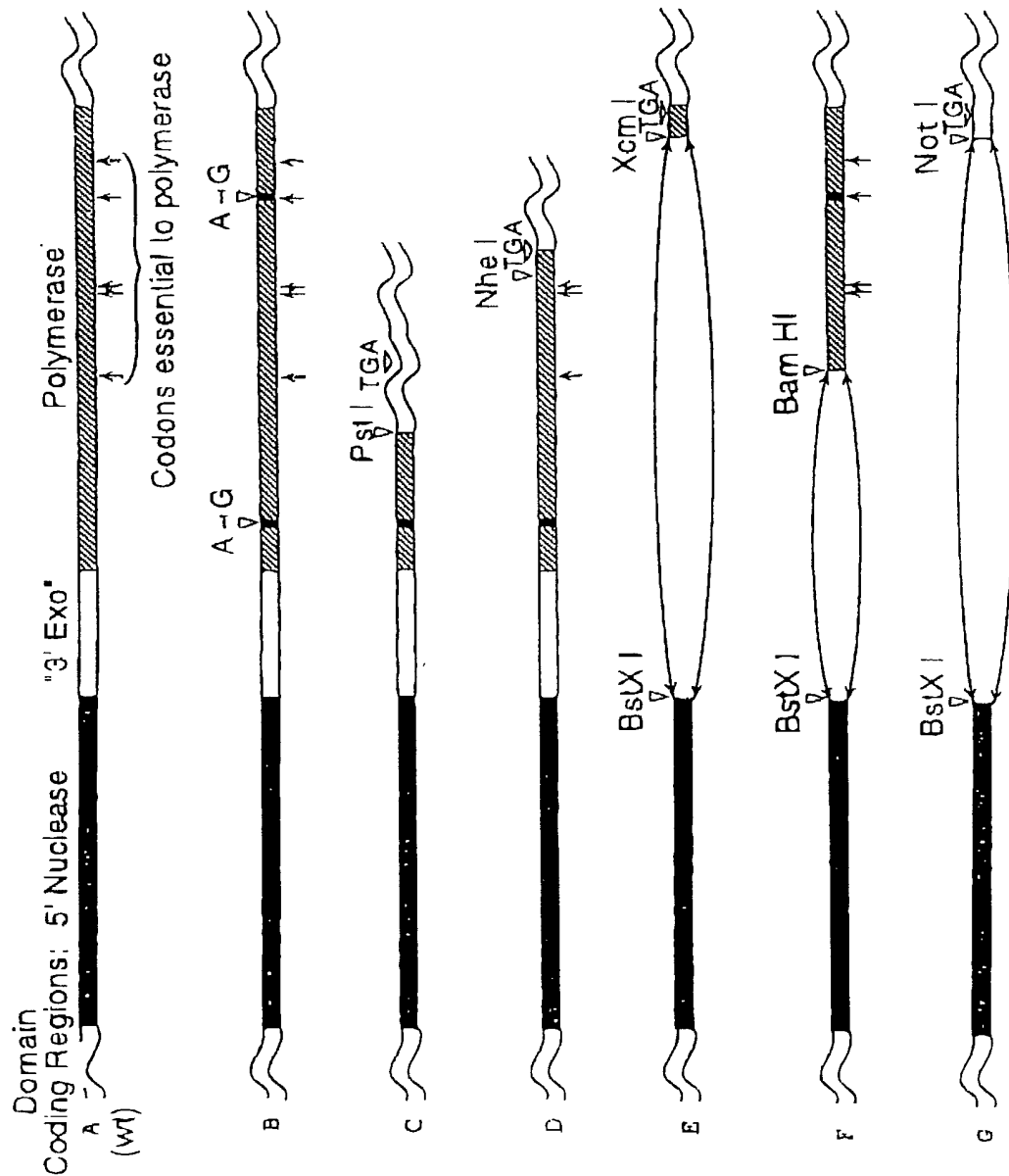


FIGURE 5

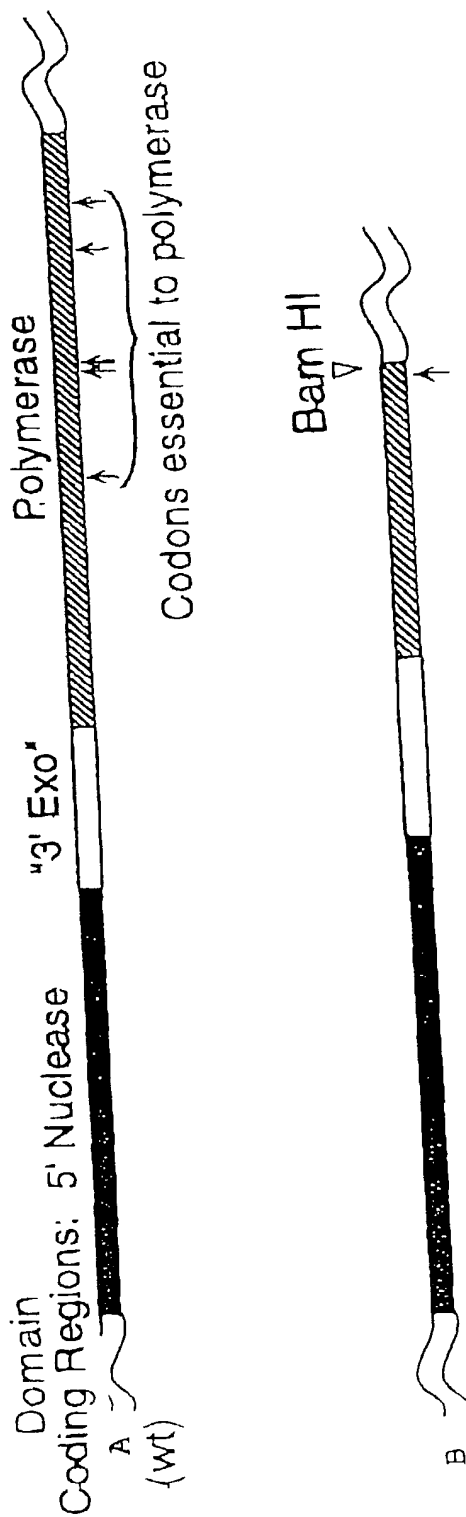
Genes for Wild-Type and Pol(-) DNAPT^H

FIGURE 6

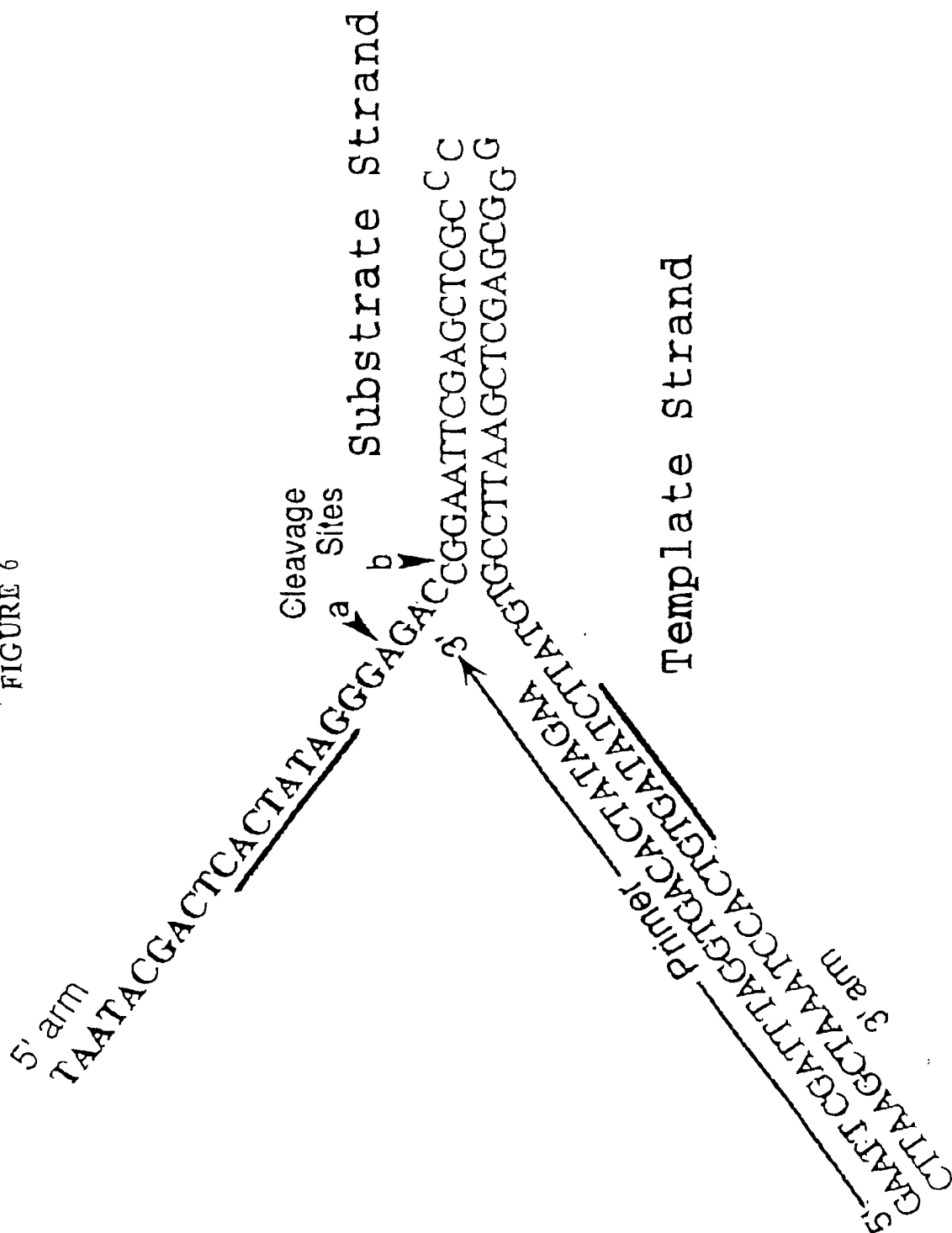


FIGURE 7

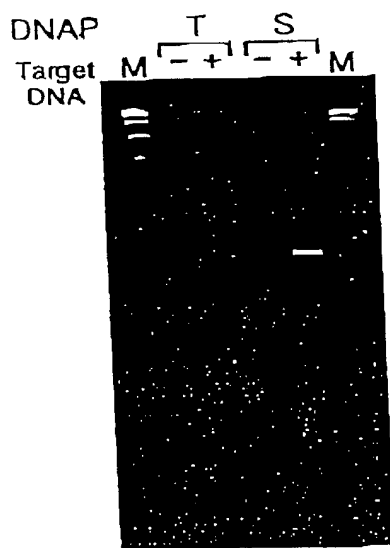


FIGURE 8

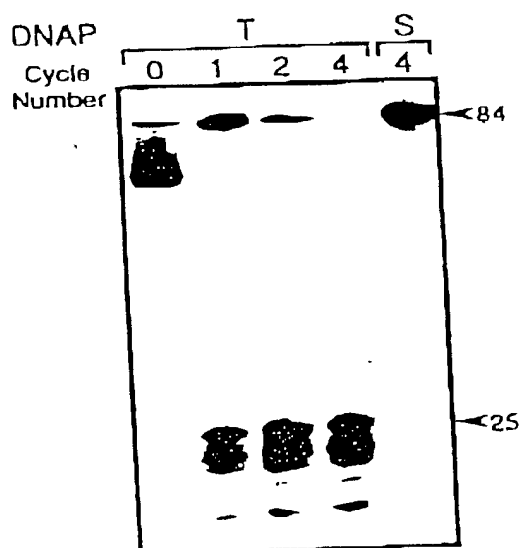


FIGURE 9

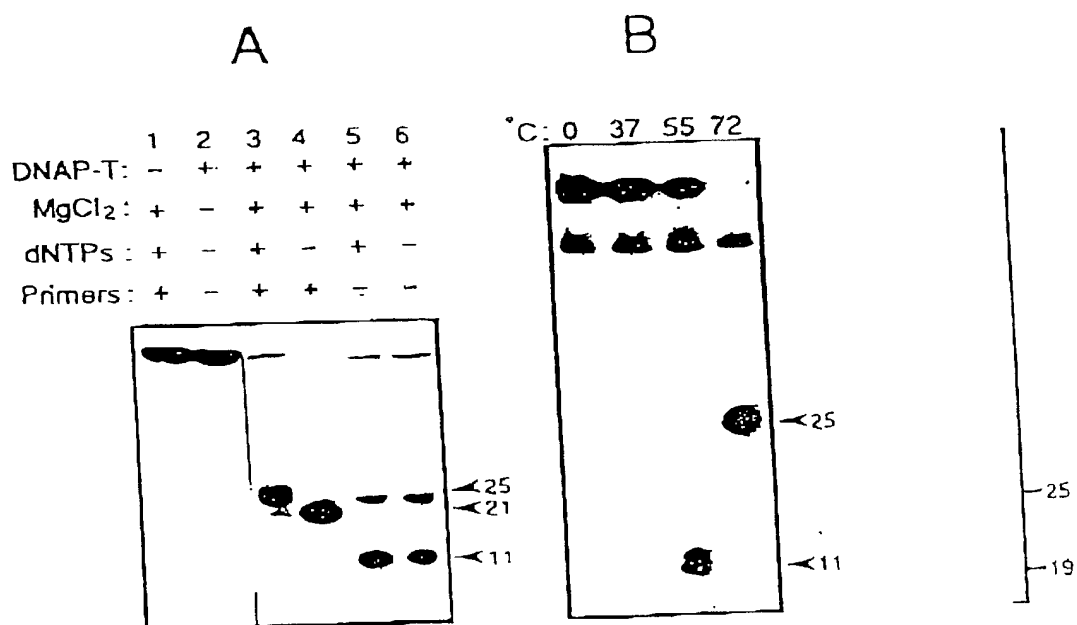


FIGURE 10

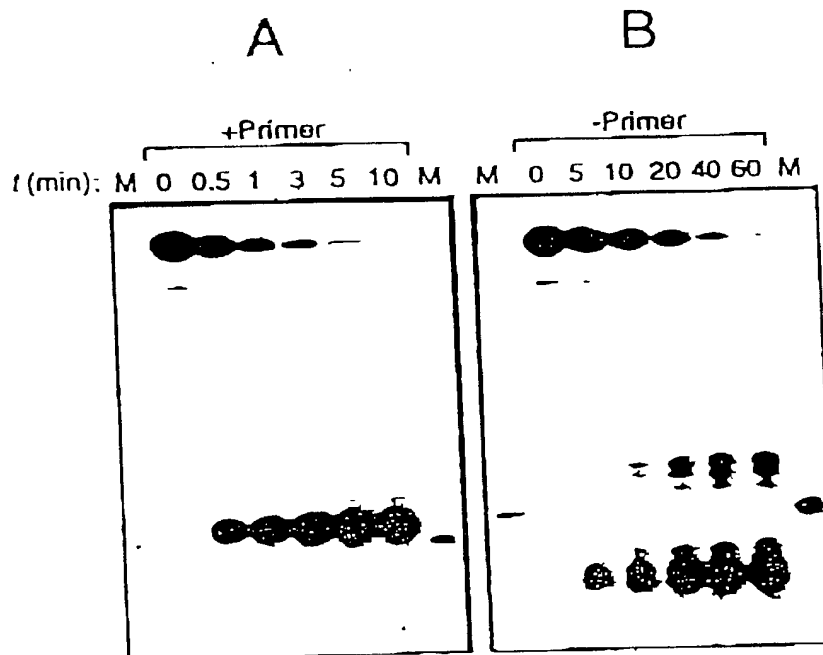


FIGURE 11

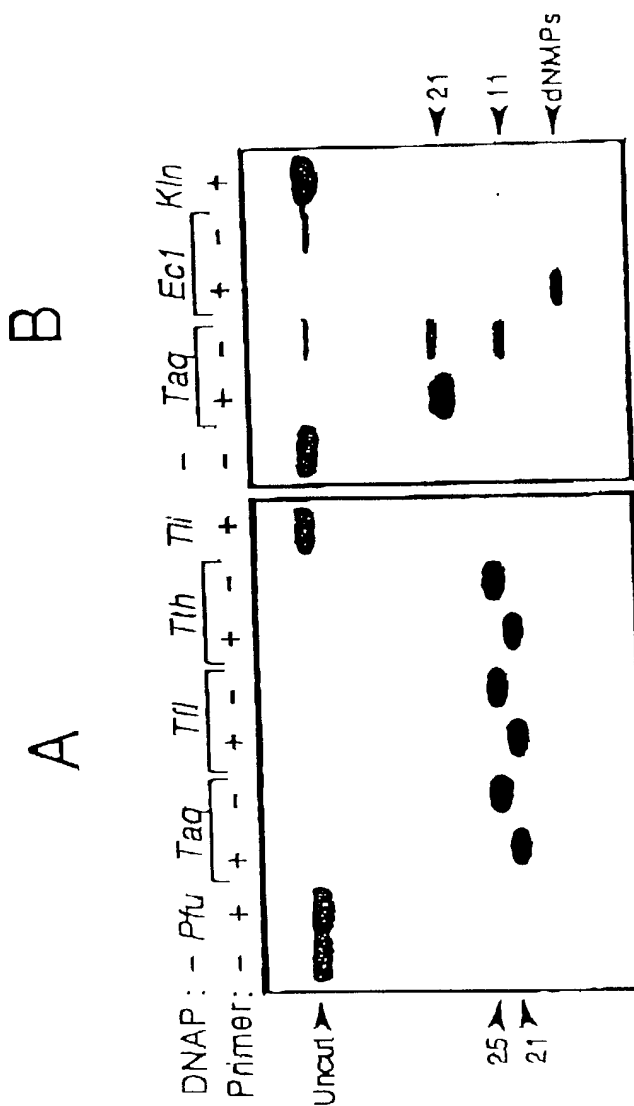


FIGURE 12

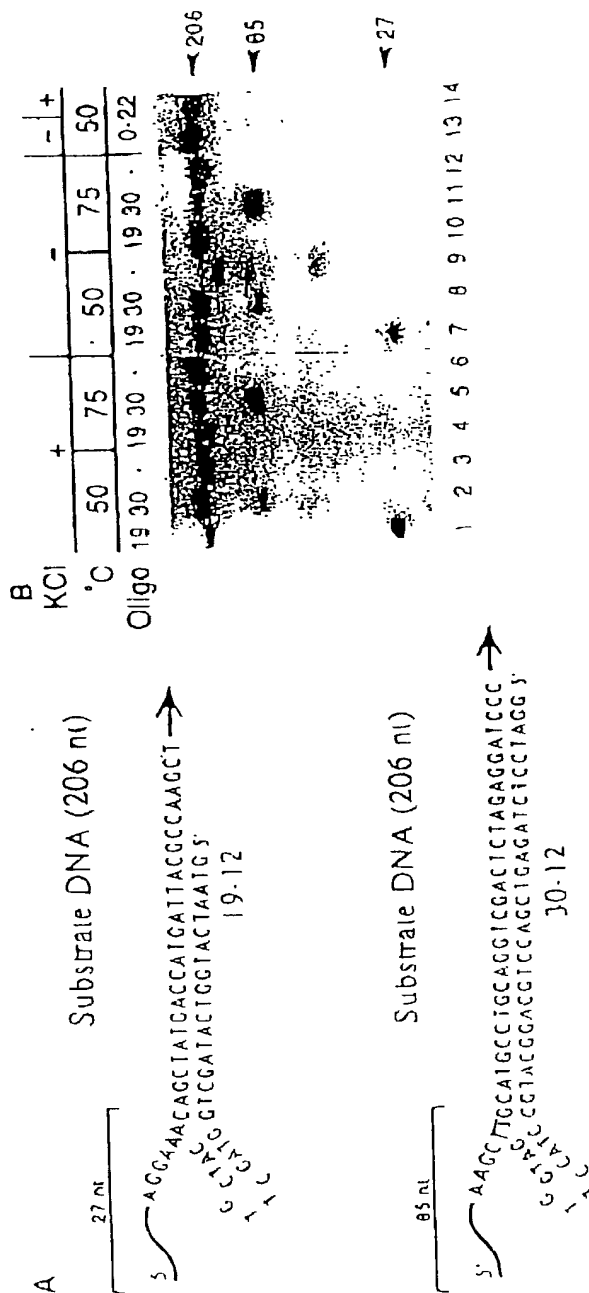


FIGURE 13

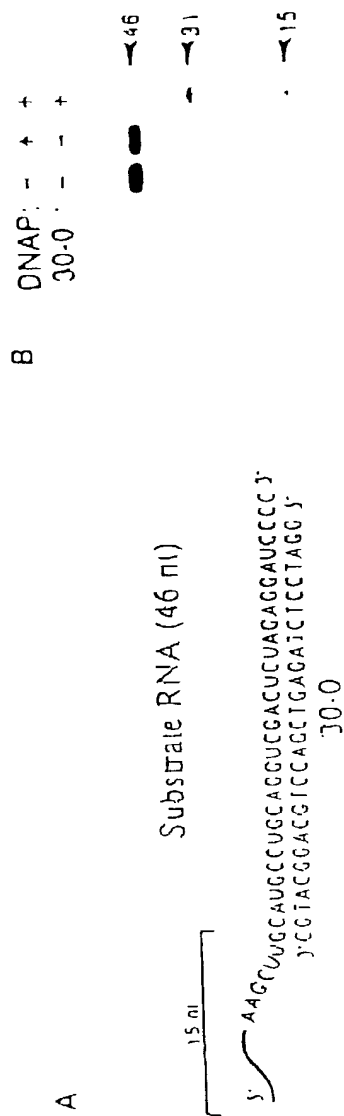


FIGURE 14

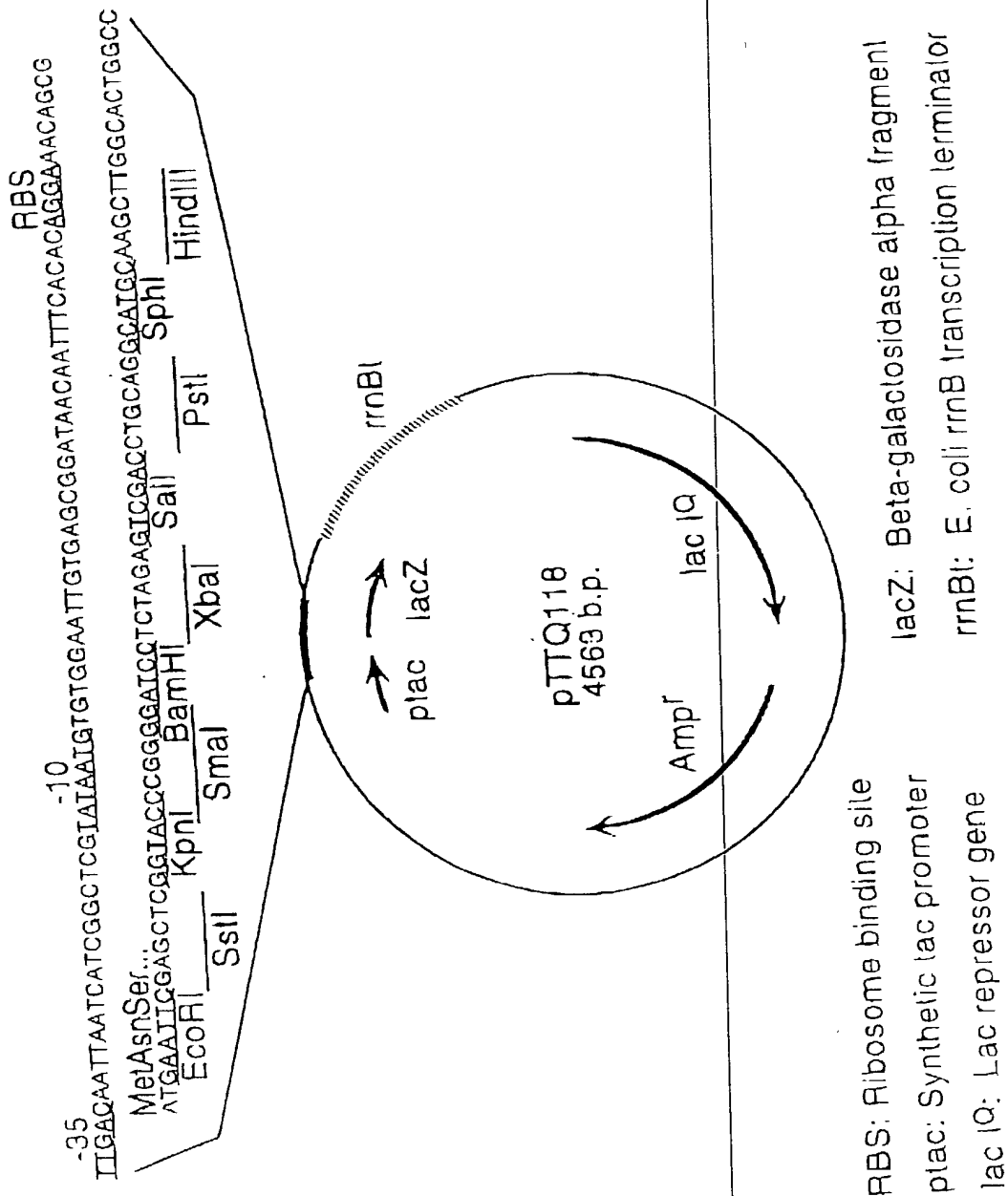
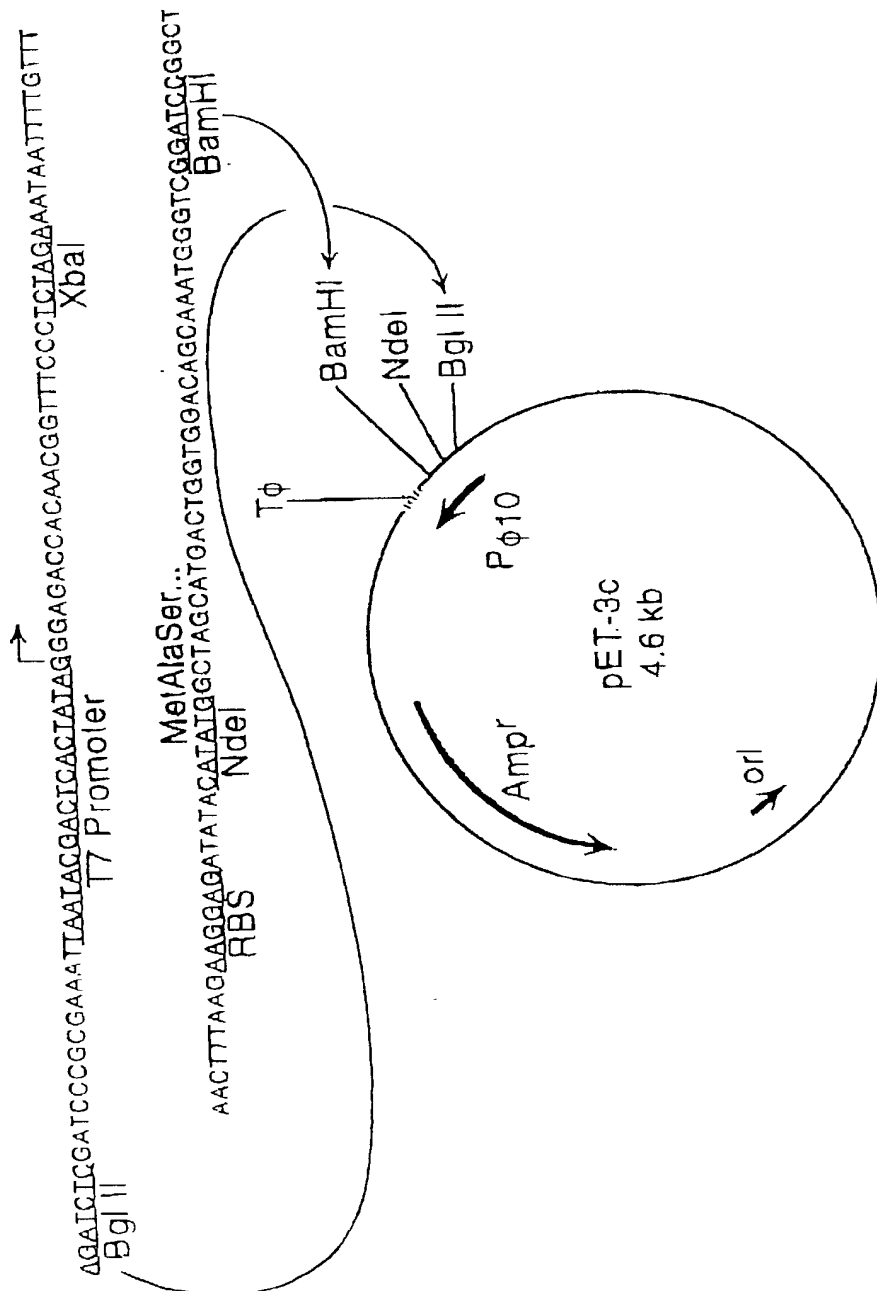


FIGURE 15



RBS: Ribosome binding site

P_{φ10}: Bacteriophage T7 $\phi 10$ promoter

T ϕ : T7 ϕ Terminator

FIGURE 16

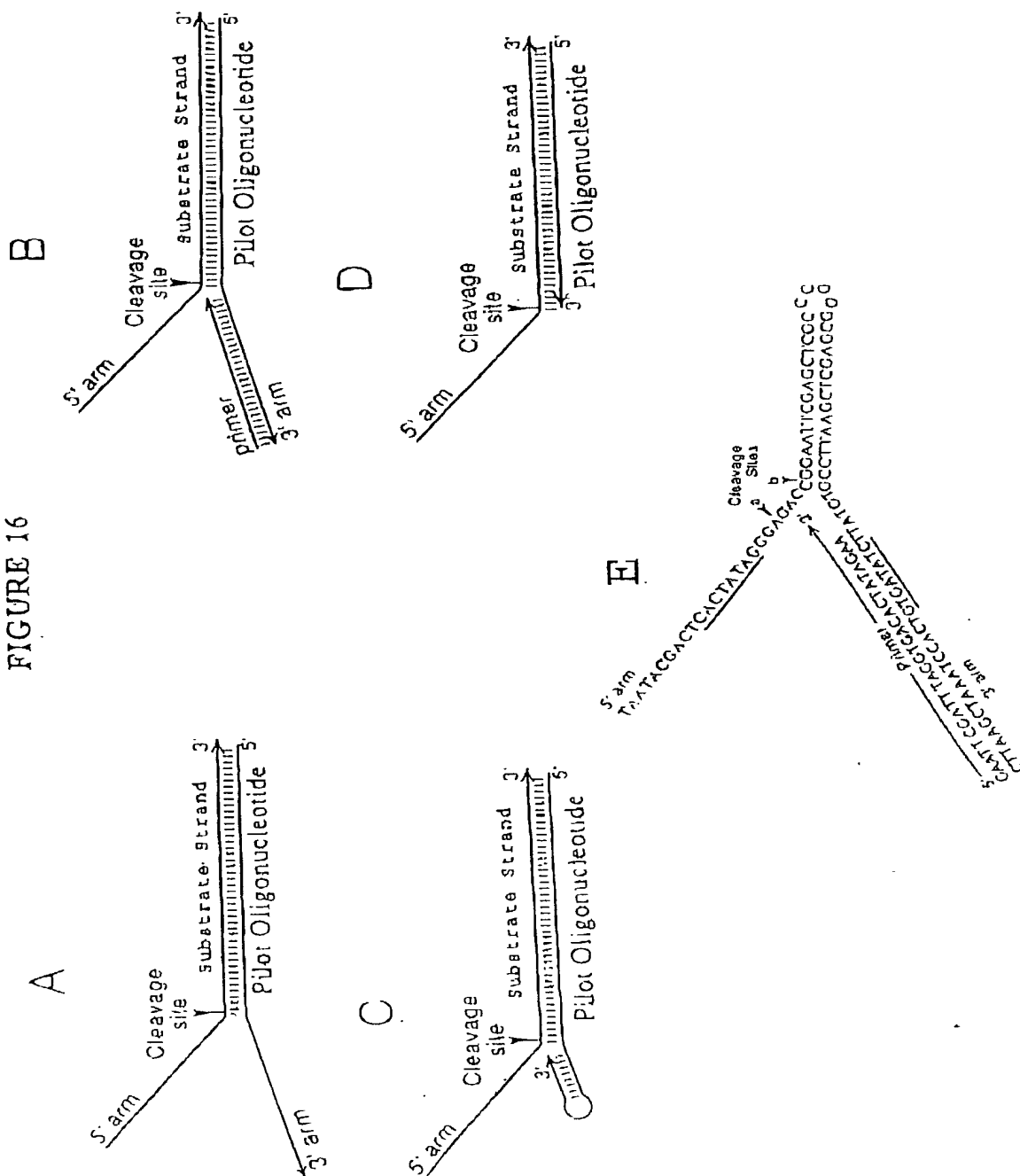


FIGURE 17

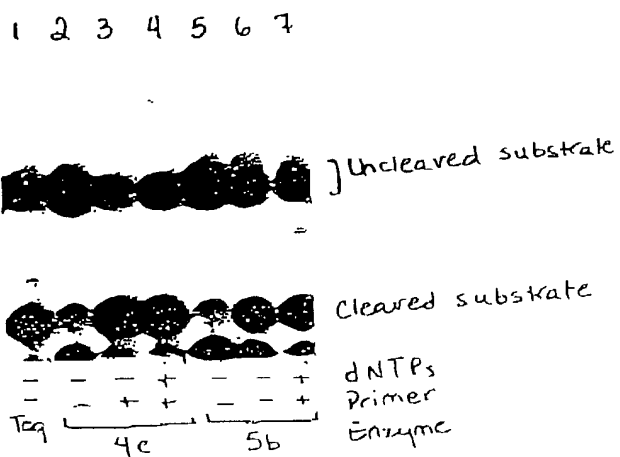


FIGURE 18

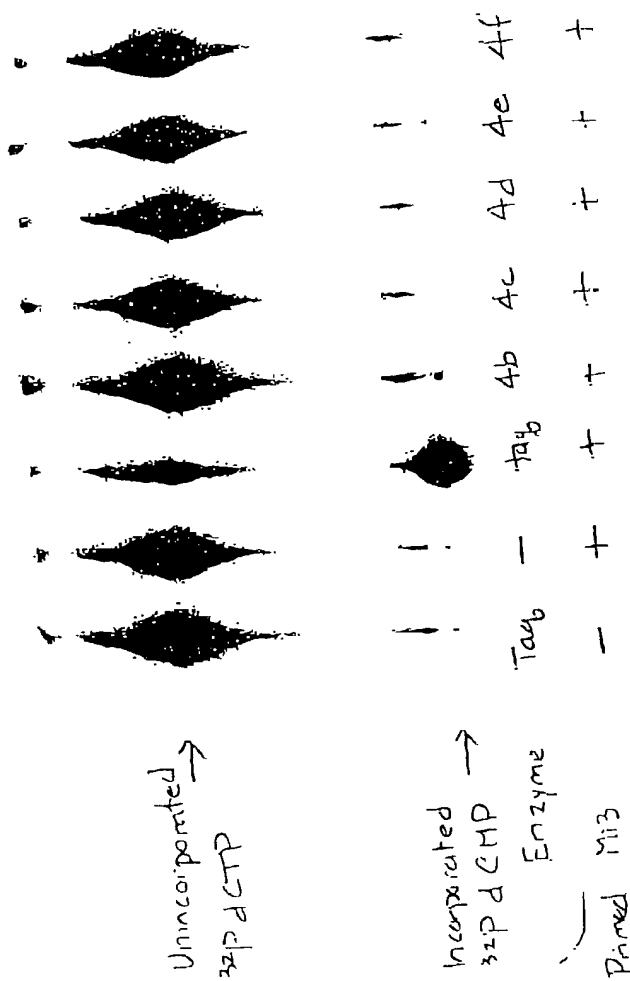
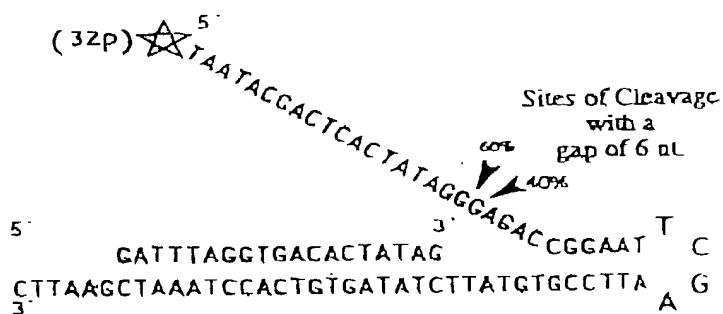


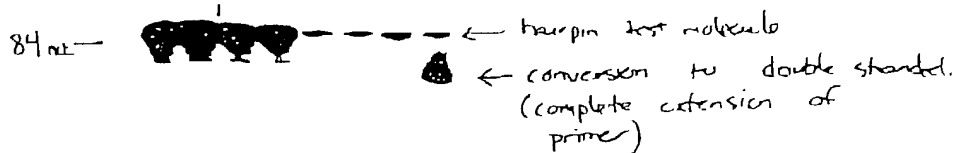
FIGURE 19

A

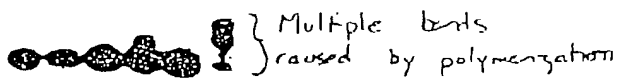


B

4d		4b		(2 pr. mutation)		Unmodified	
No		Rel.		small		DNAP Tag	
Activity		Activity		Activity		Activity	
1	2	3	4	5	6	7	8
C +		T +		T +		T +	
-		-		-		-	



desired product →
 21 nuc.



↑ some aberrant cleavage with
 4b" because of residual
 polymerase activity.

Top = T-Hairpin
Bottom = A-Hairpin

BsmI

Rsa I
Mnl I
Nla III
Hgi I
Nla IV
Rsa I
Kpn I

BsmI

CTTTCTGCTGTGTCCTCTCTCTTGGCCCTTGTAACCATGTGGTACCTGTGTGCGTGTCTCAGCTTGTTCGTC

72

FIGURE 22A

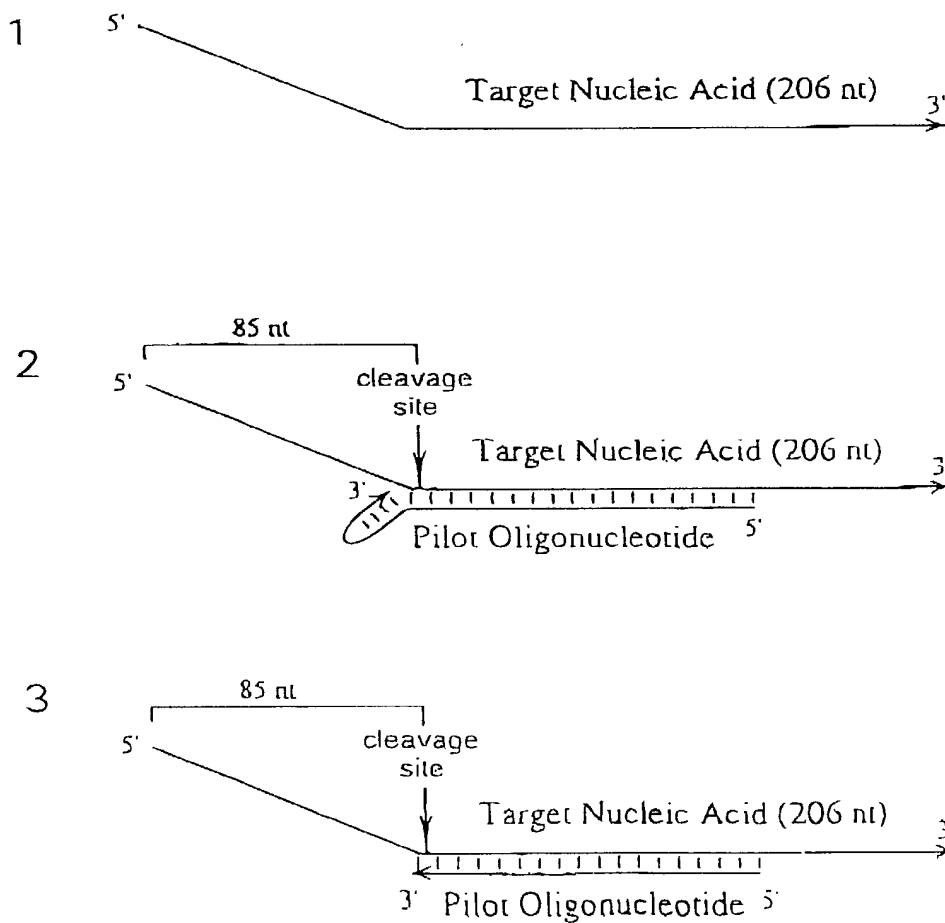


FIGURE 22B

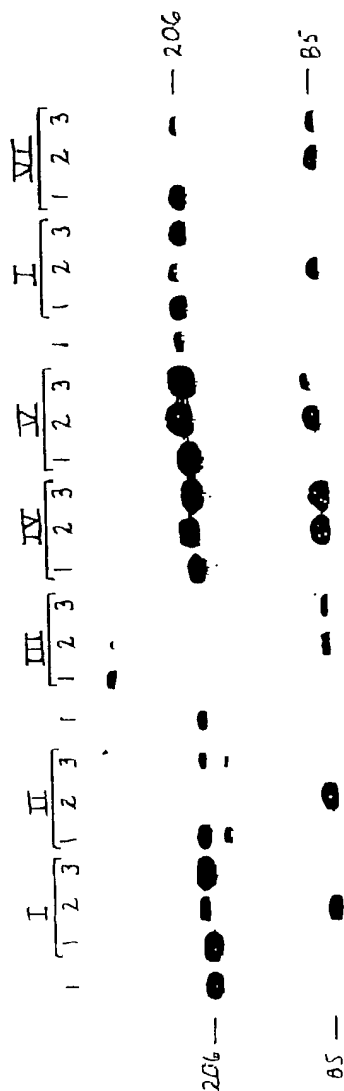


FIGURE 23

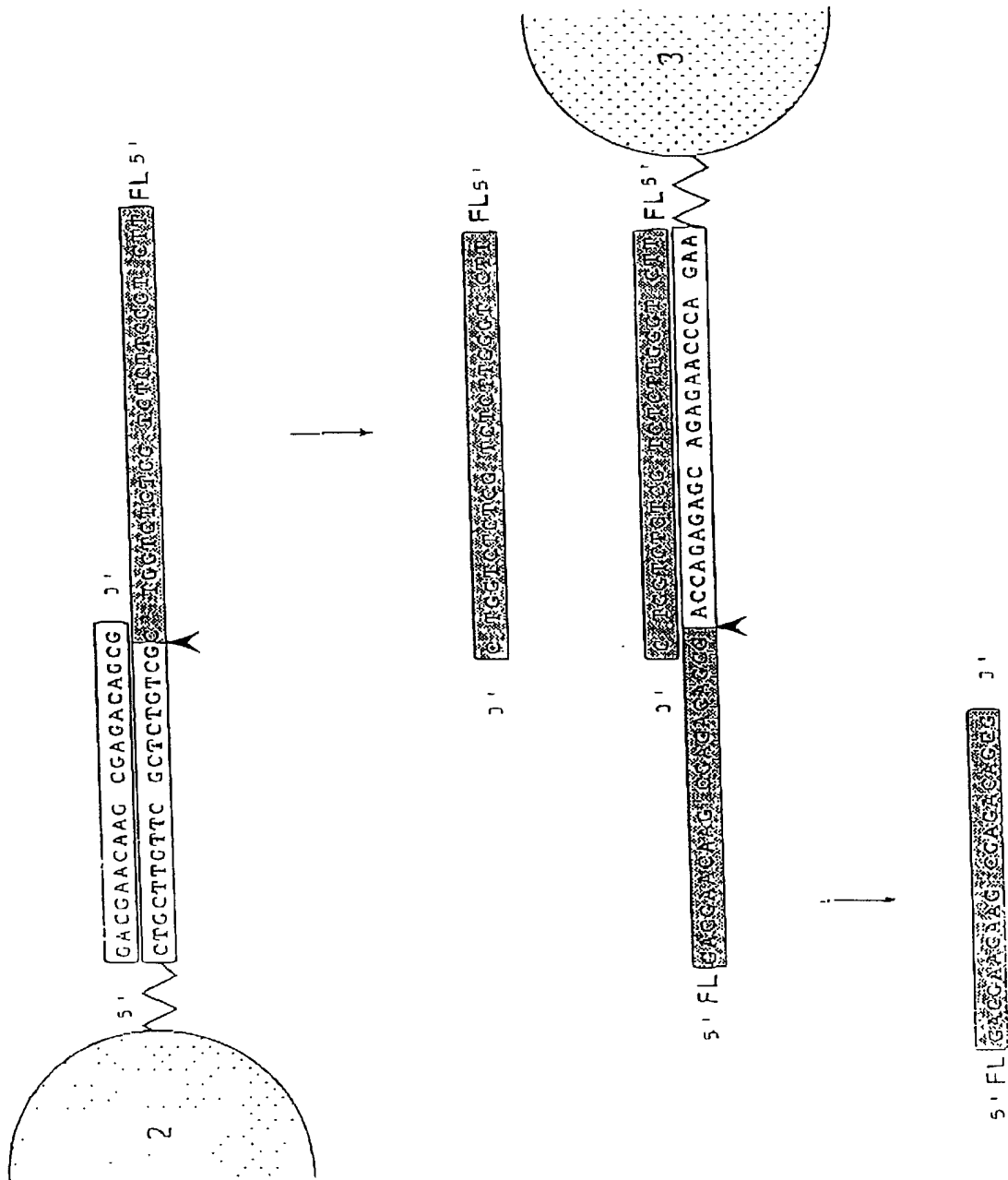


FIGURE 25

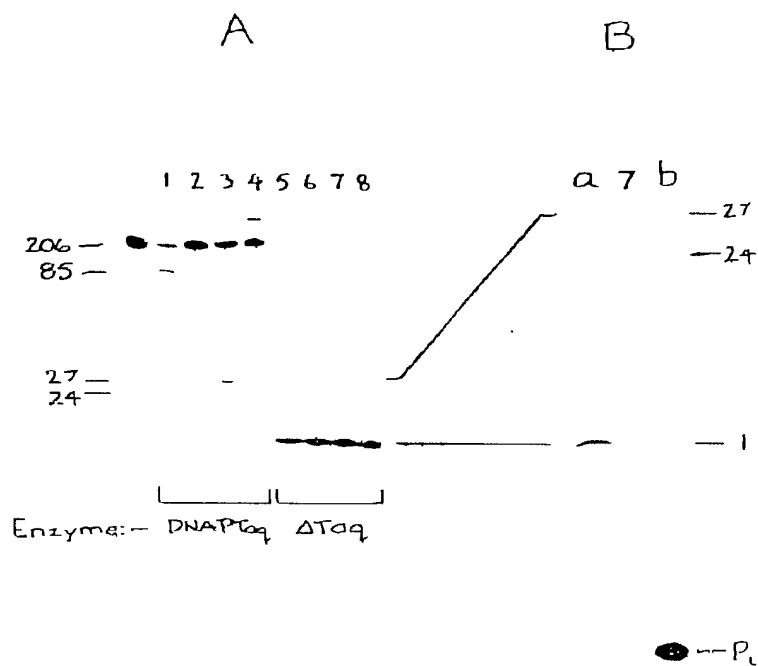
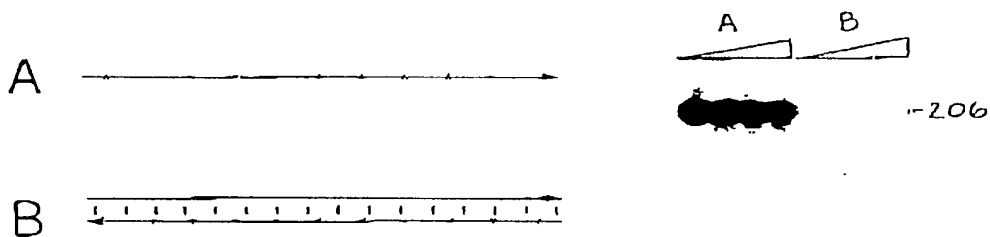


FIGURE 26



$\cdot = {}^{32}\text{P}$

FIGURE 27

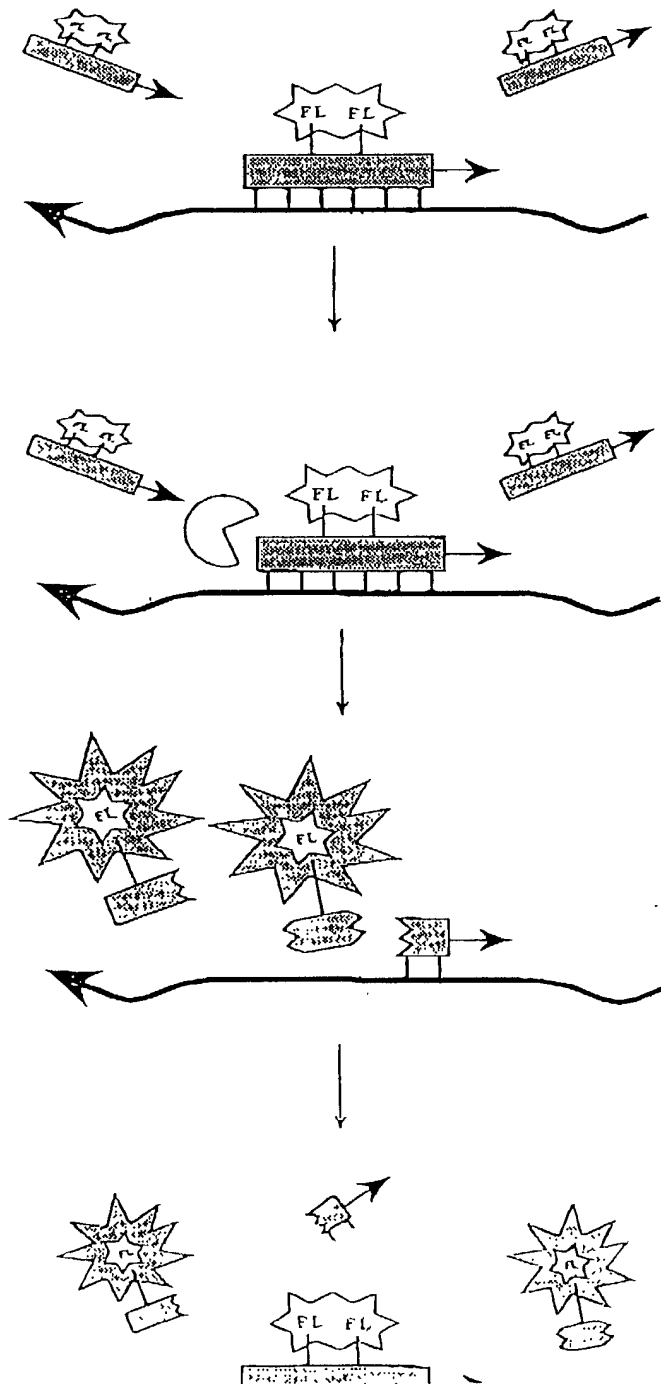


FIGURE 28B

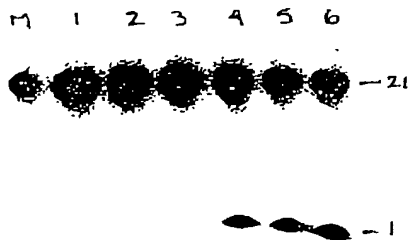


FIGURE 29

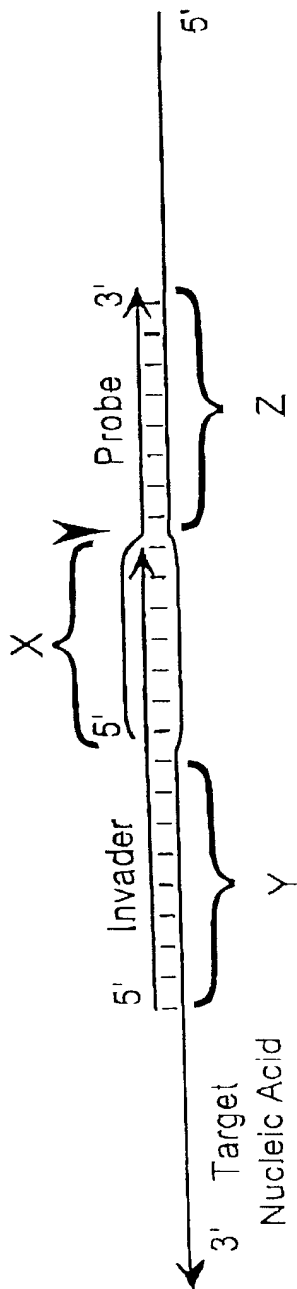


FIGURE 30

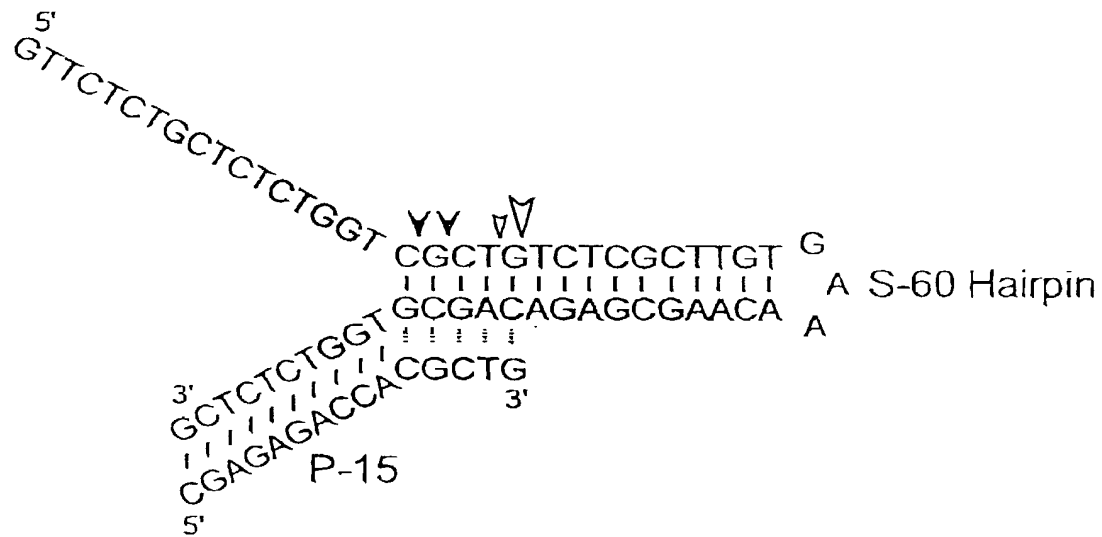


FIGURE 31

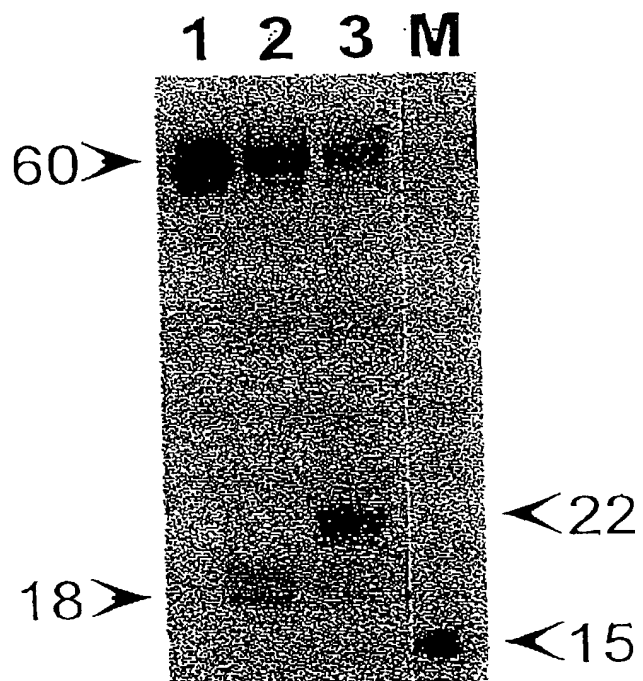
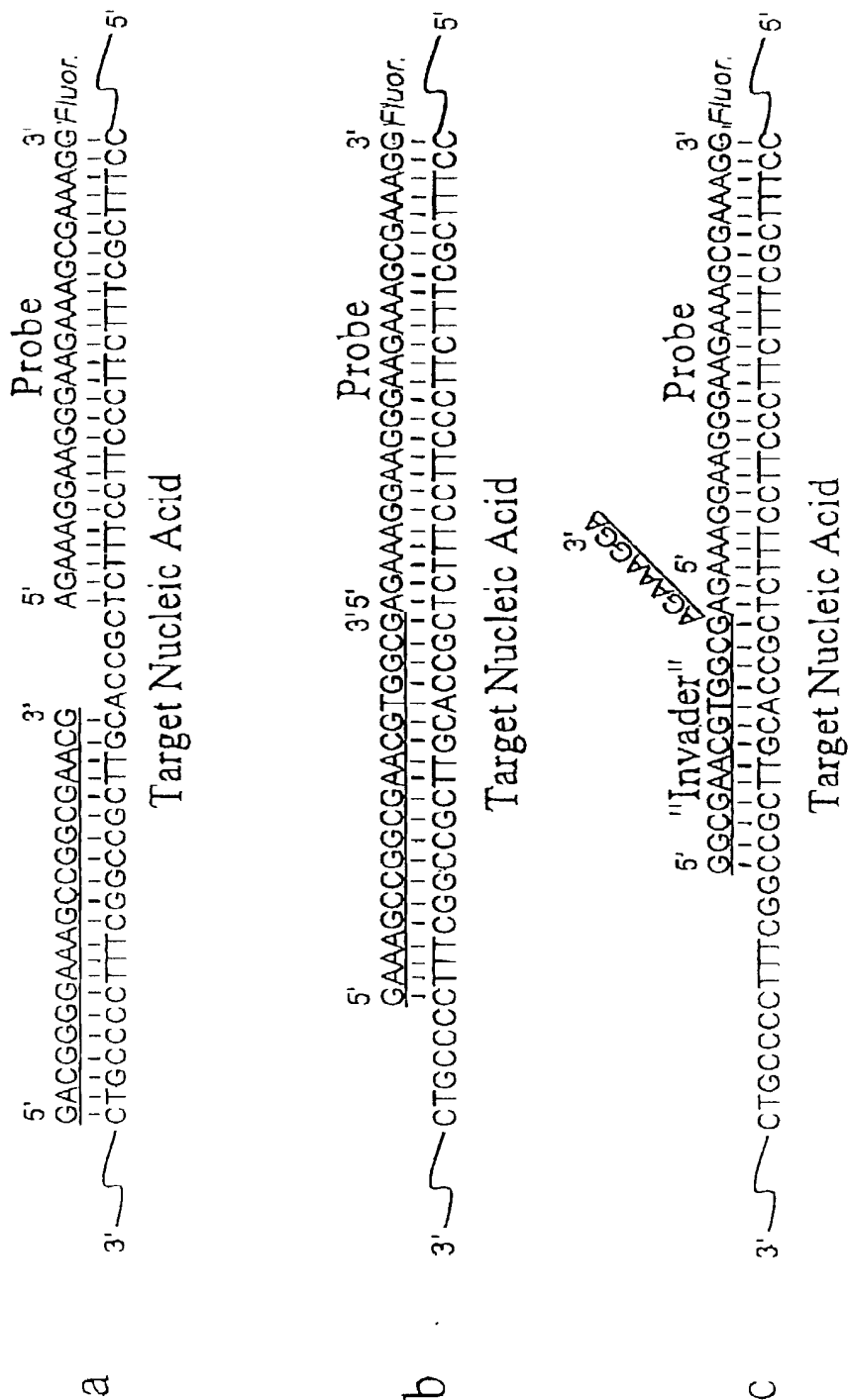


FIGURE 32





4

9

5

4

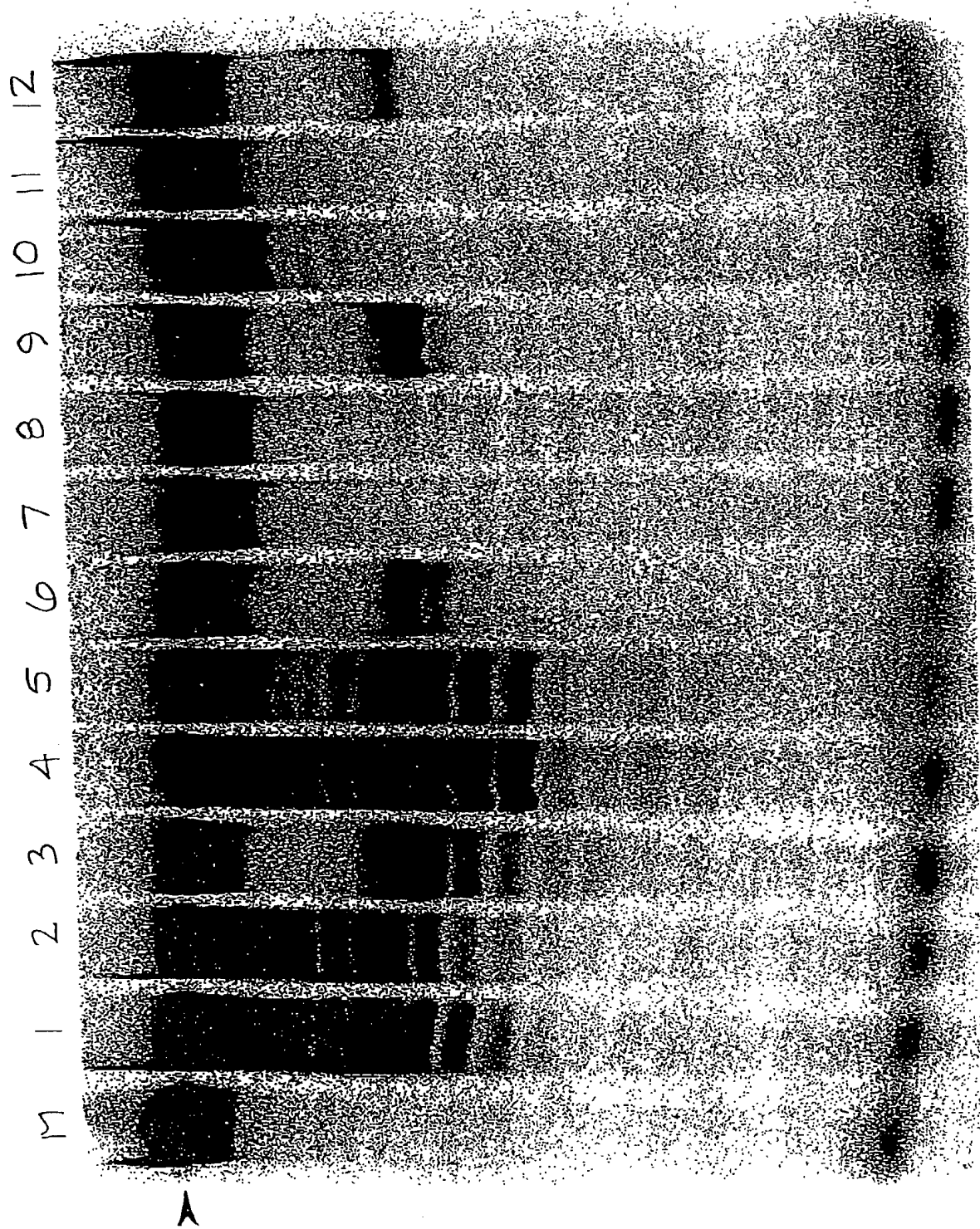
3

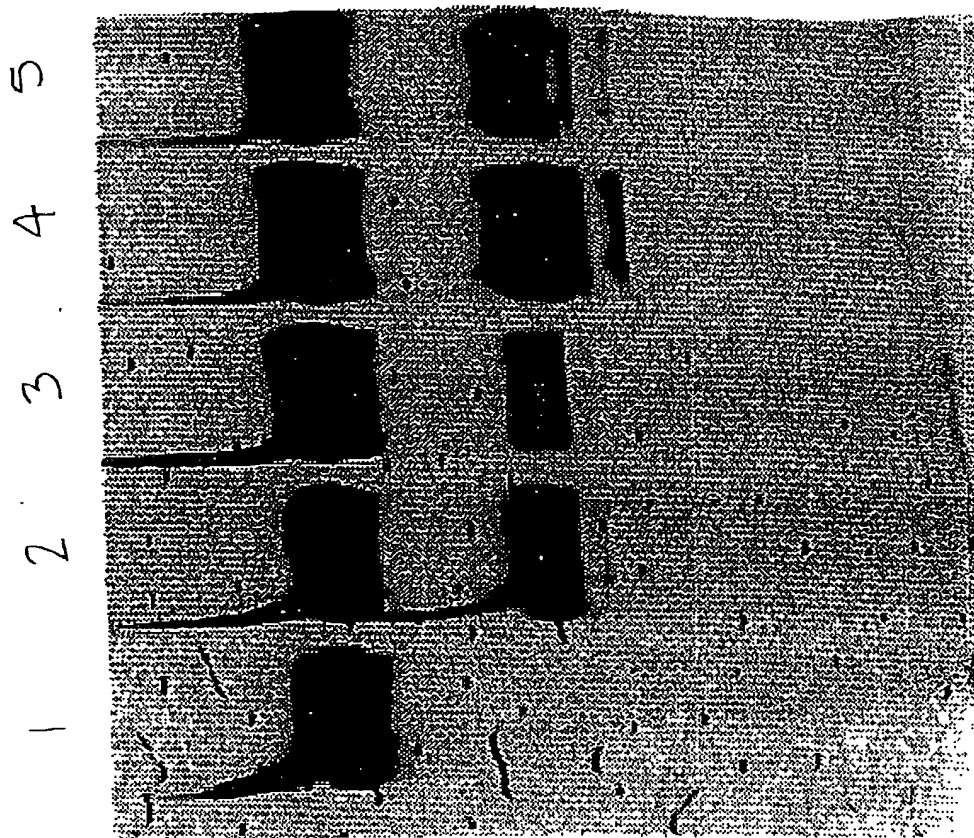
2

A 2

45

FIGURE 34





26 A

FIGURE 36

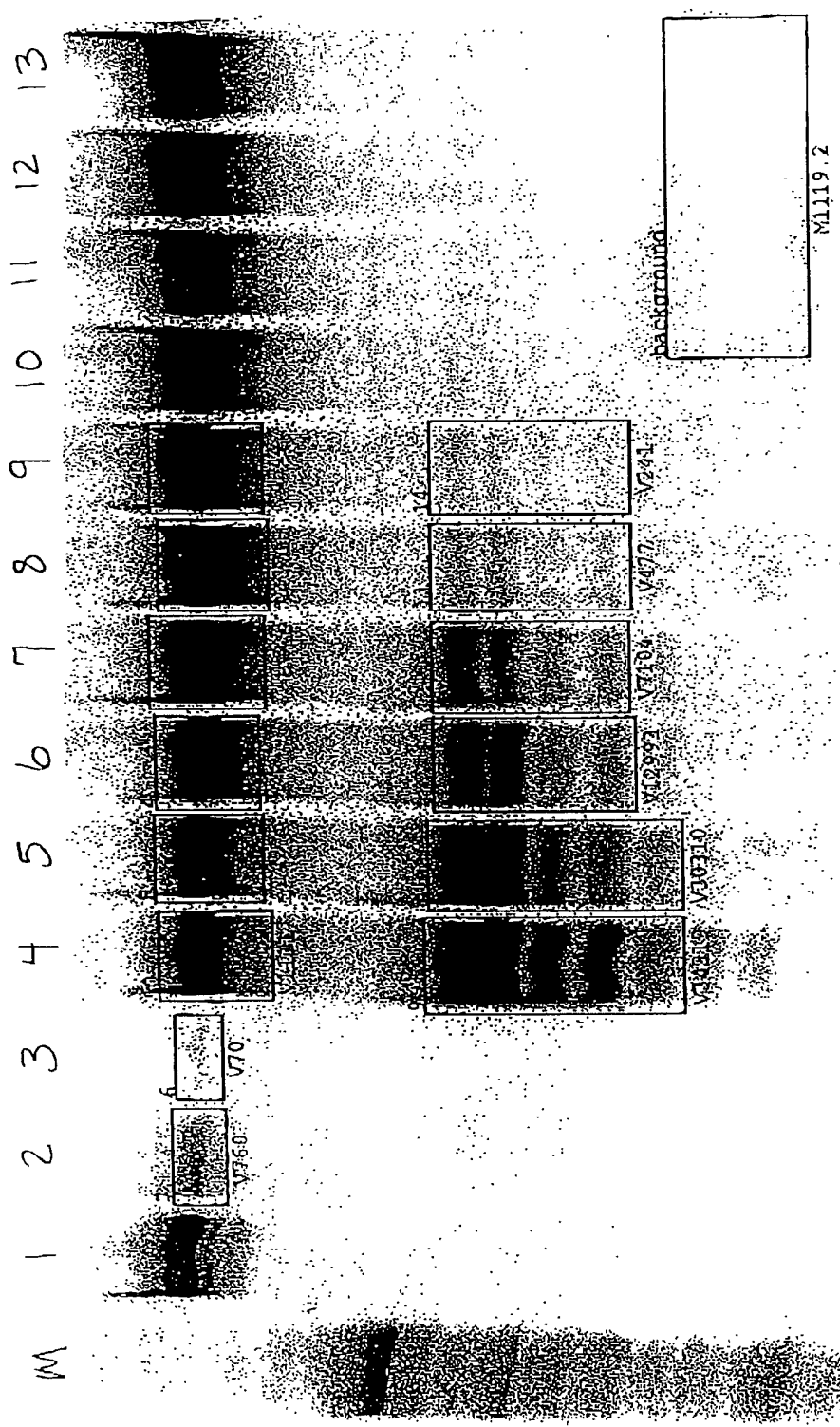


FIGURE 38

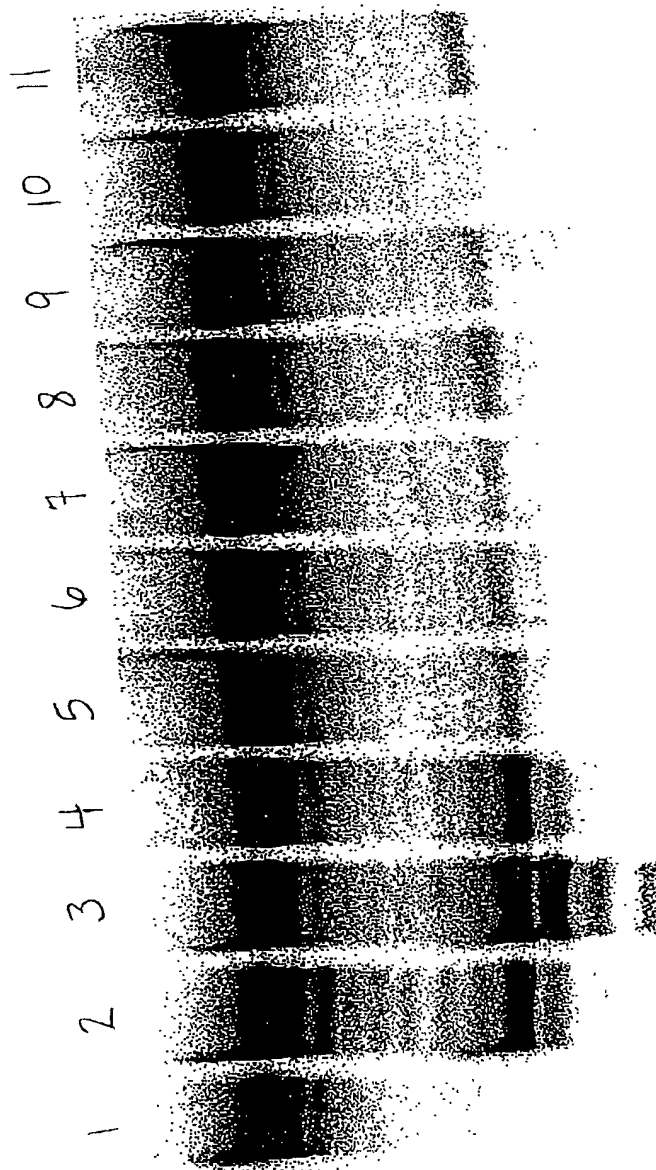


FIGURE 39

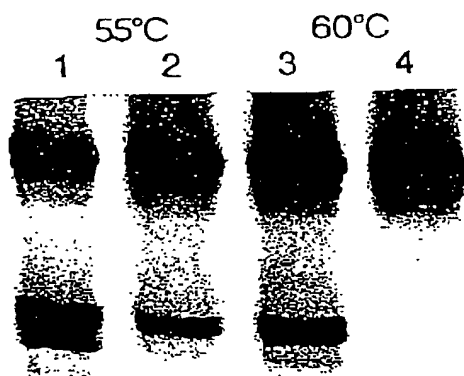


FIGURE 40

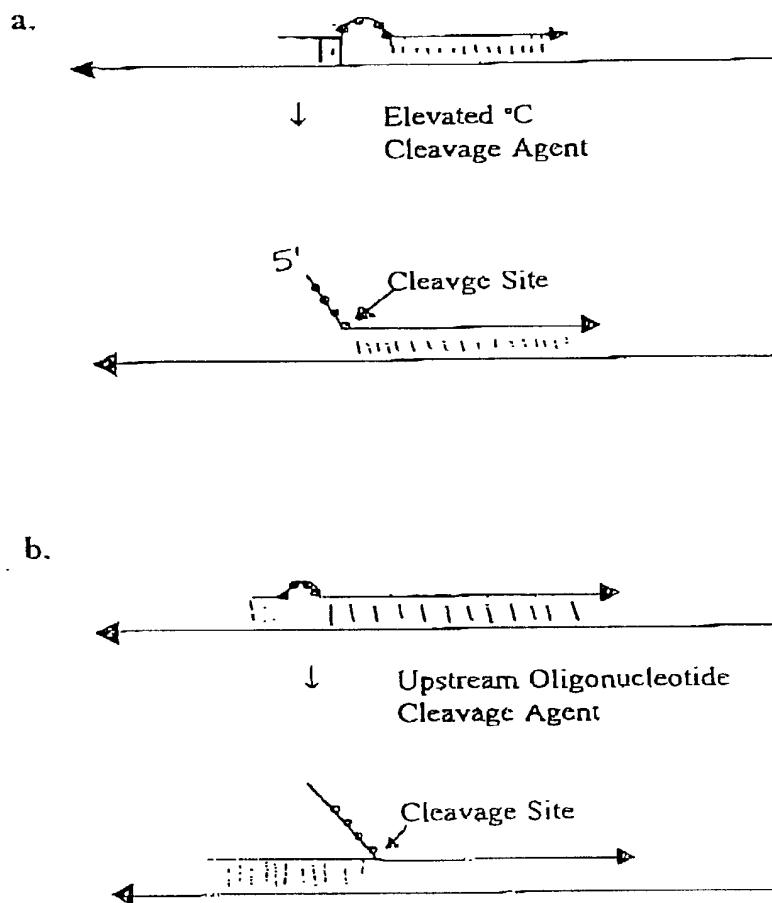


FIGURE 41

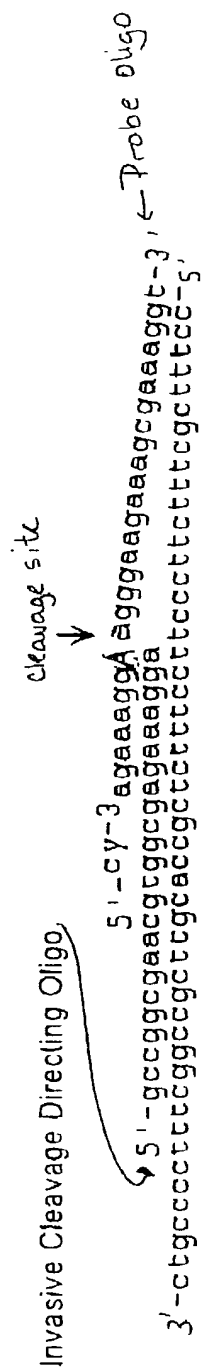


FIGURE 42

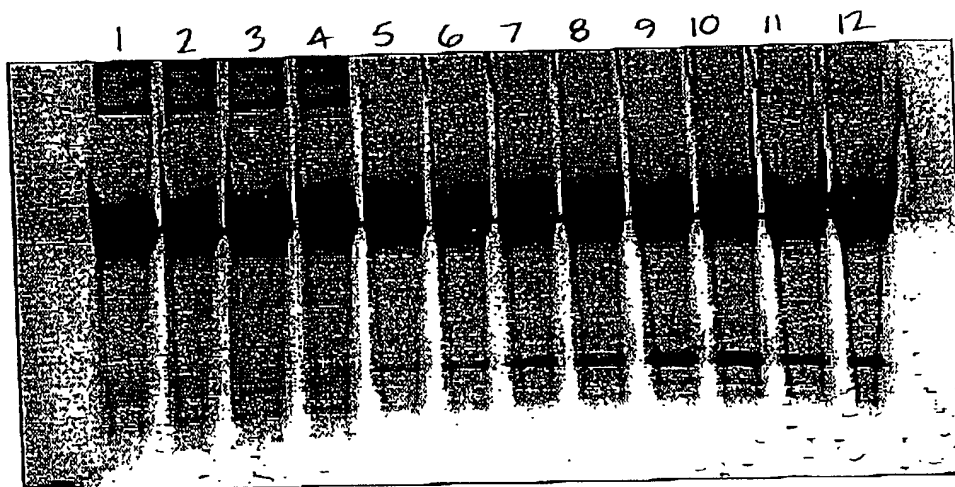


FIGURE 43

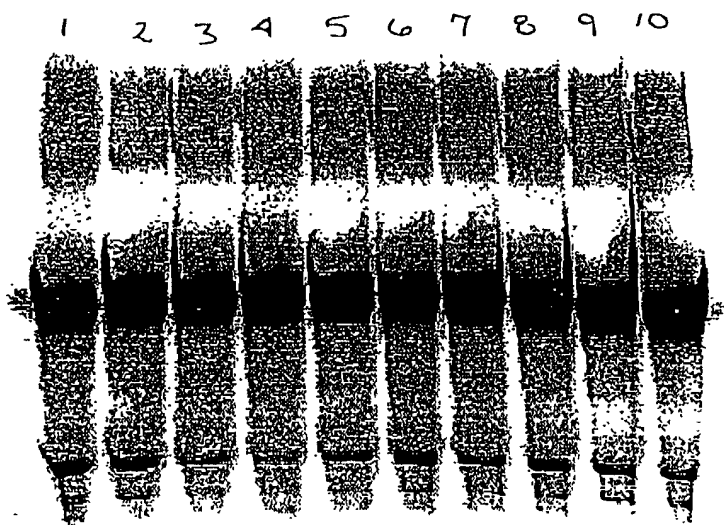


FIGURE 44

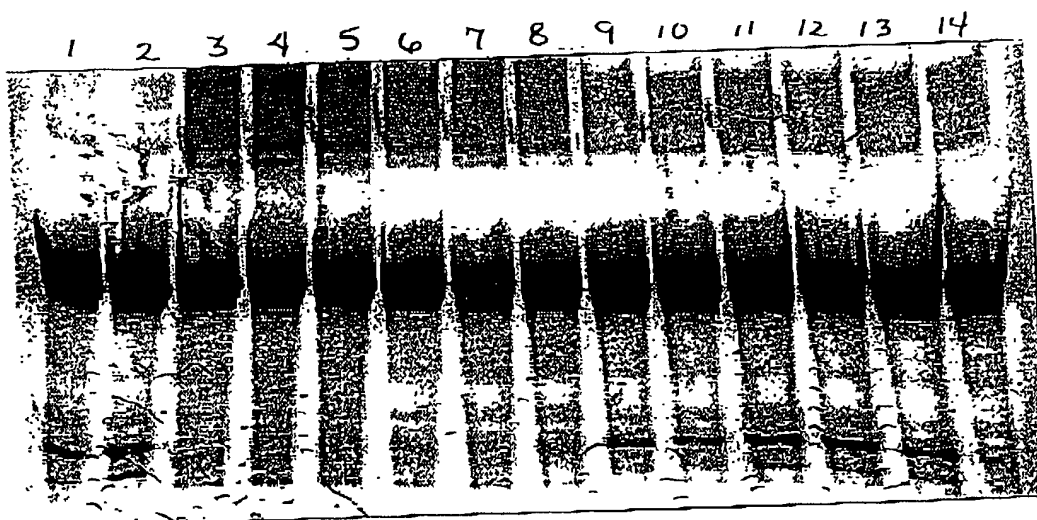


FIGURE 45

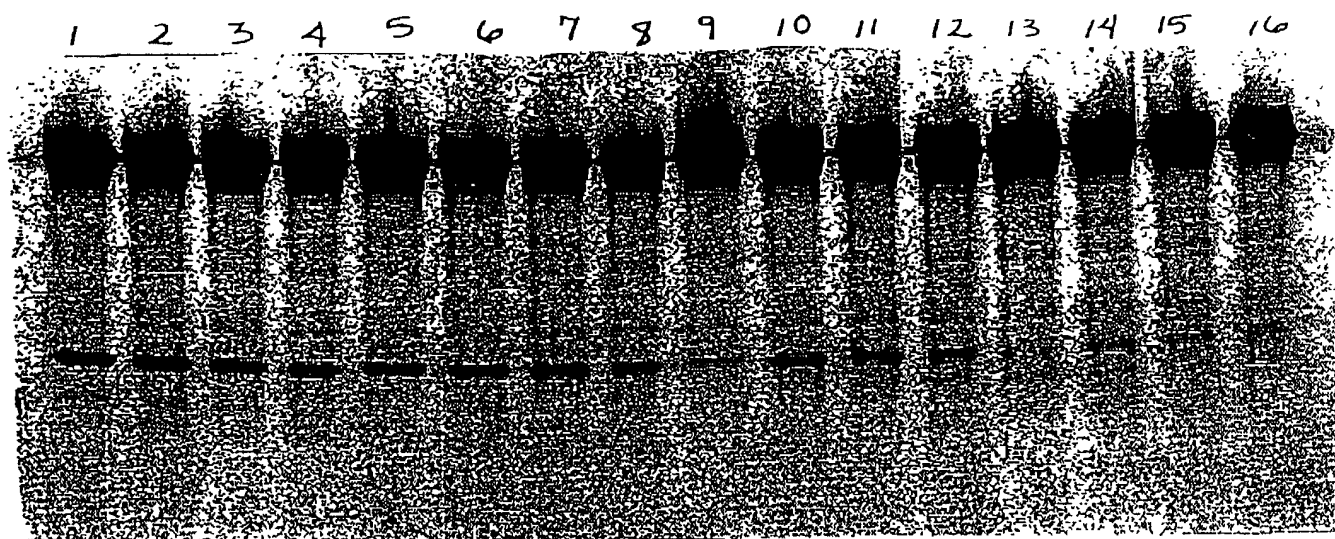


FIGURE 46

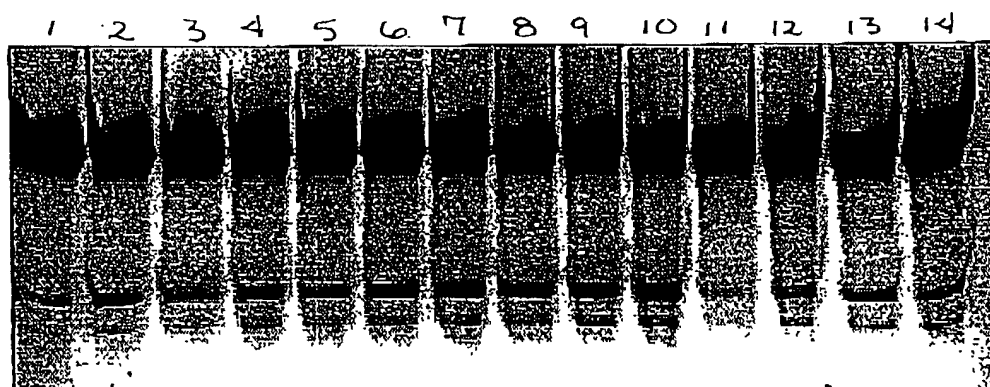


FIGURE 47

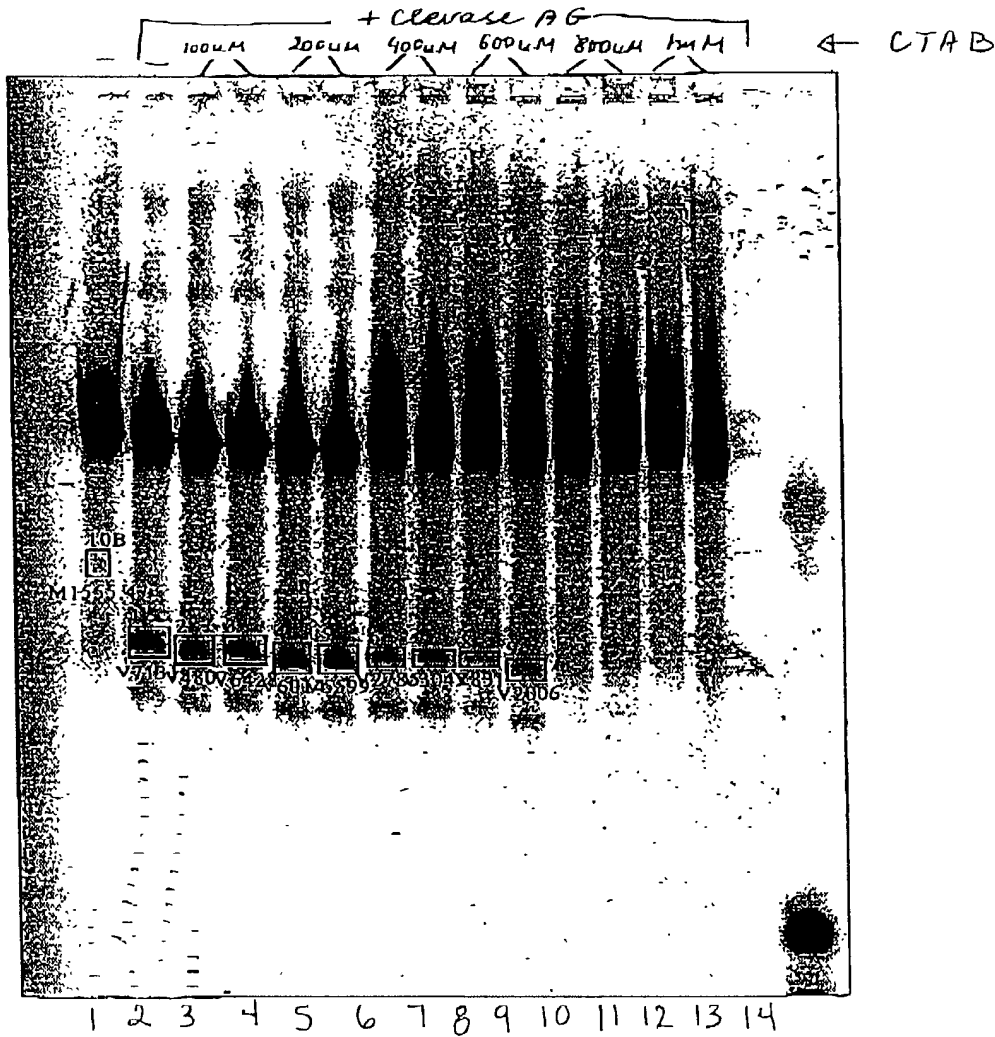


FIGURE 48

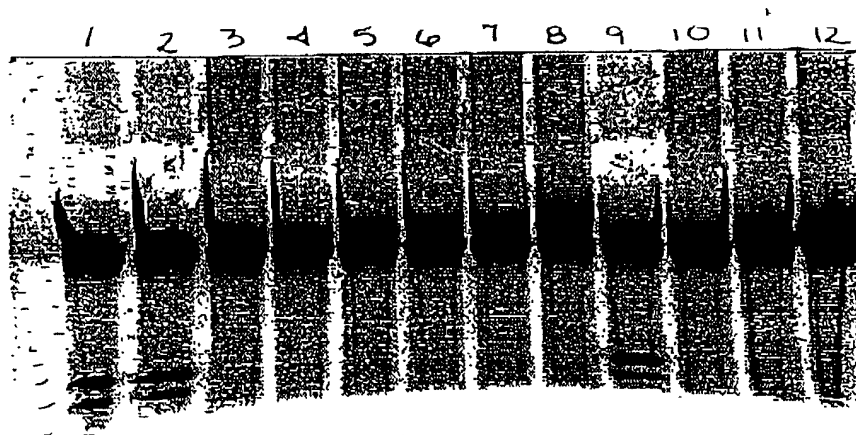


FIGURE 49

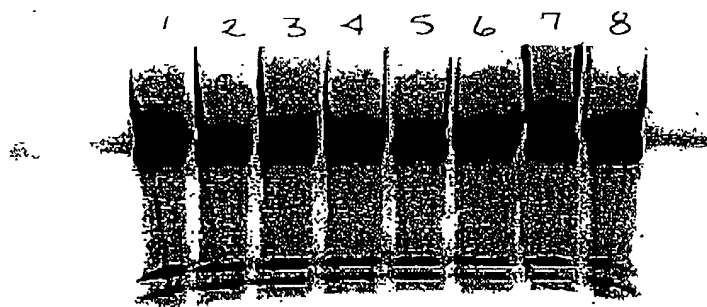


FIGURE 50

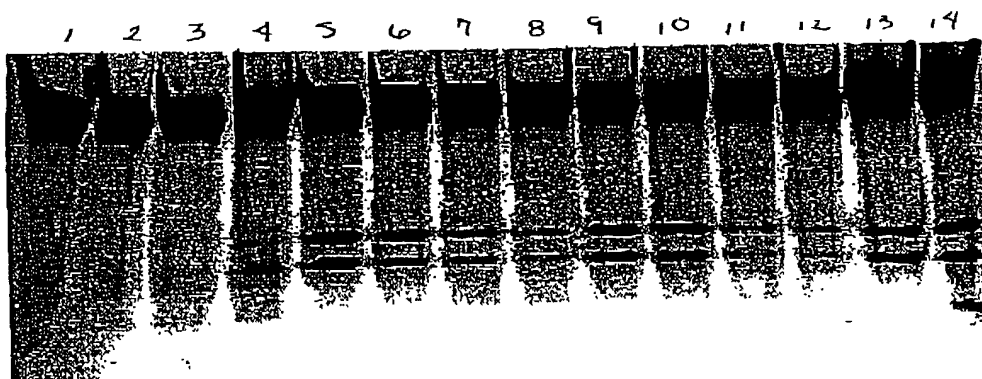


FIGURE 51

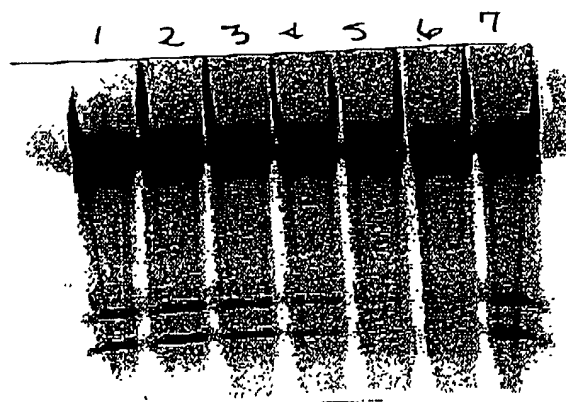


FIGURE 52

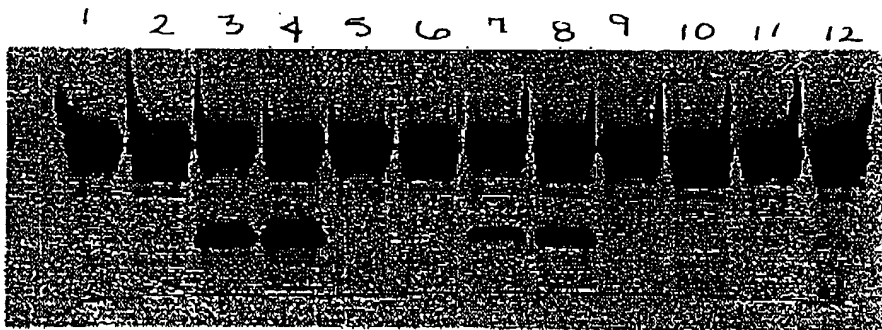


FIGURE 53

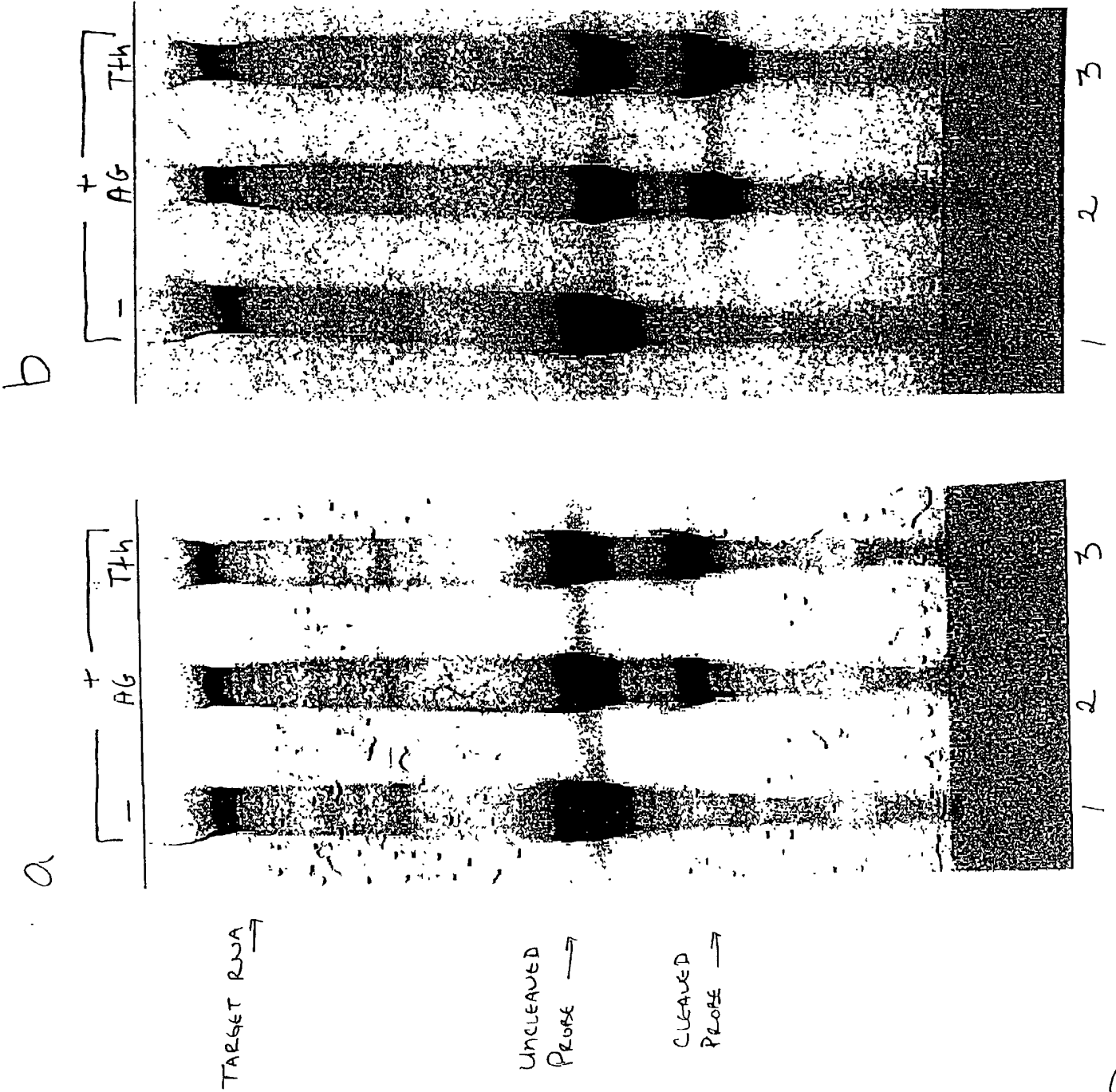


FIGURE 54

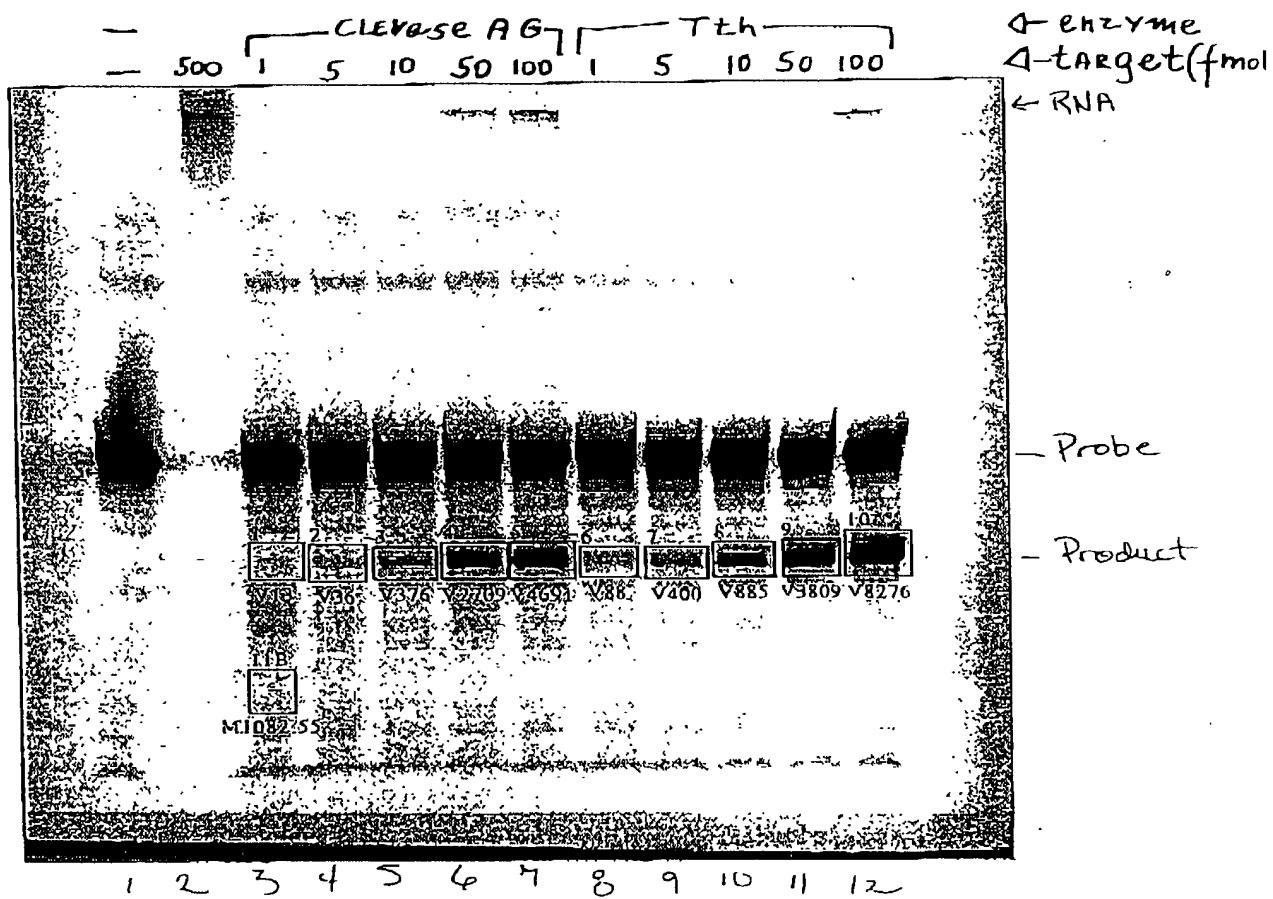


FIGURE 55

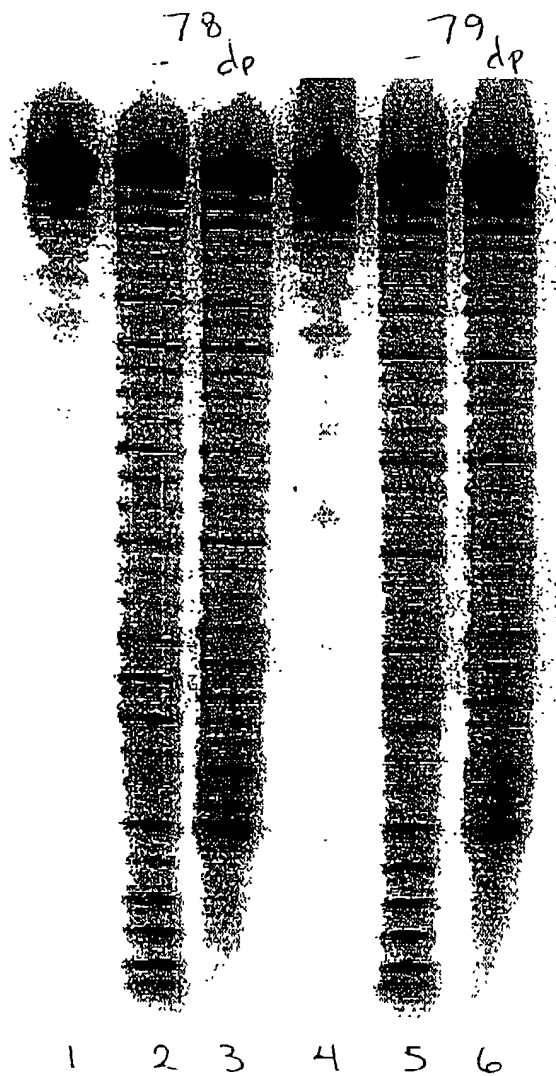


FIGURE 56

70 (C10 aminoT's)

74 (C6 amino T's)

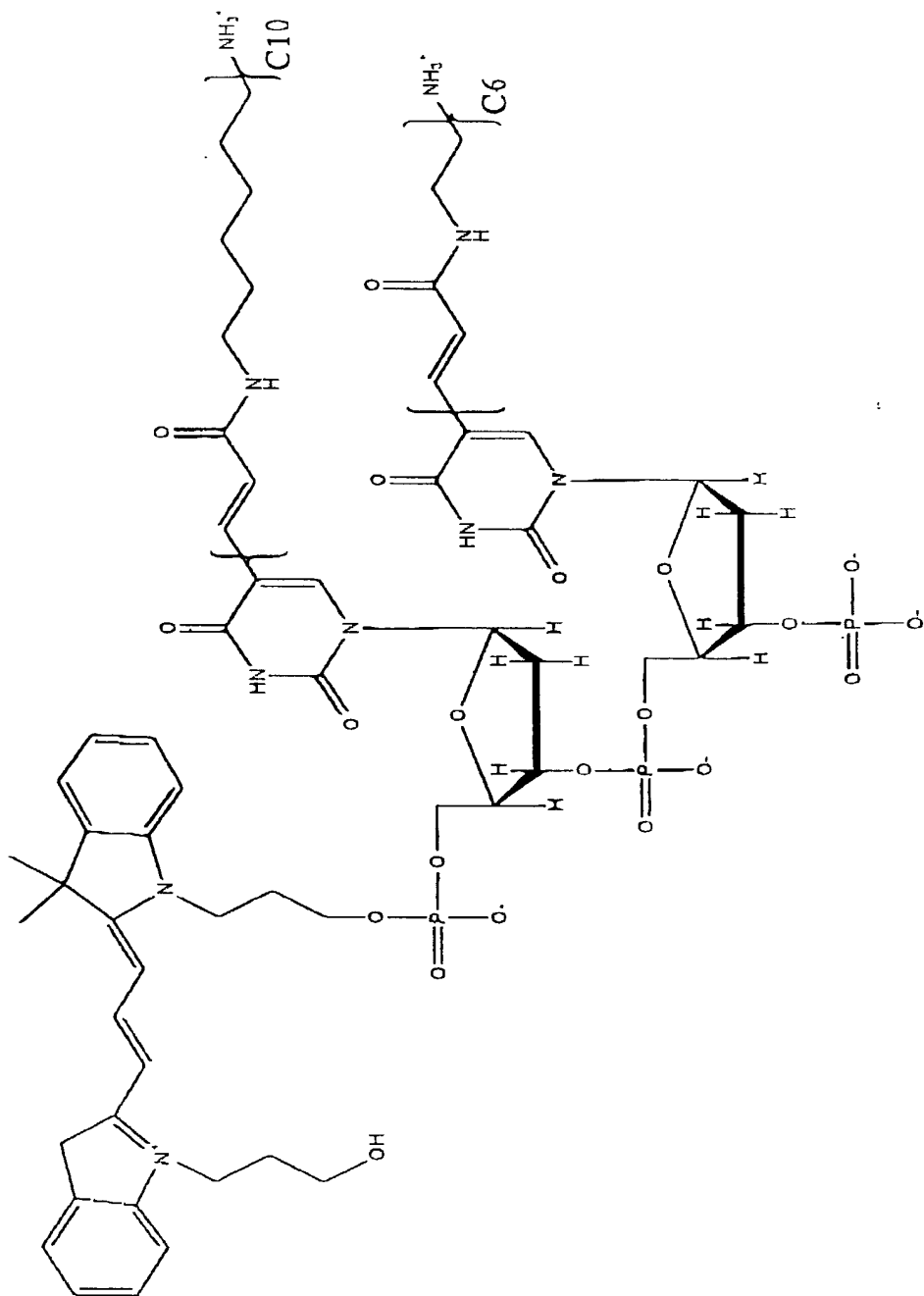
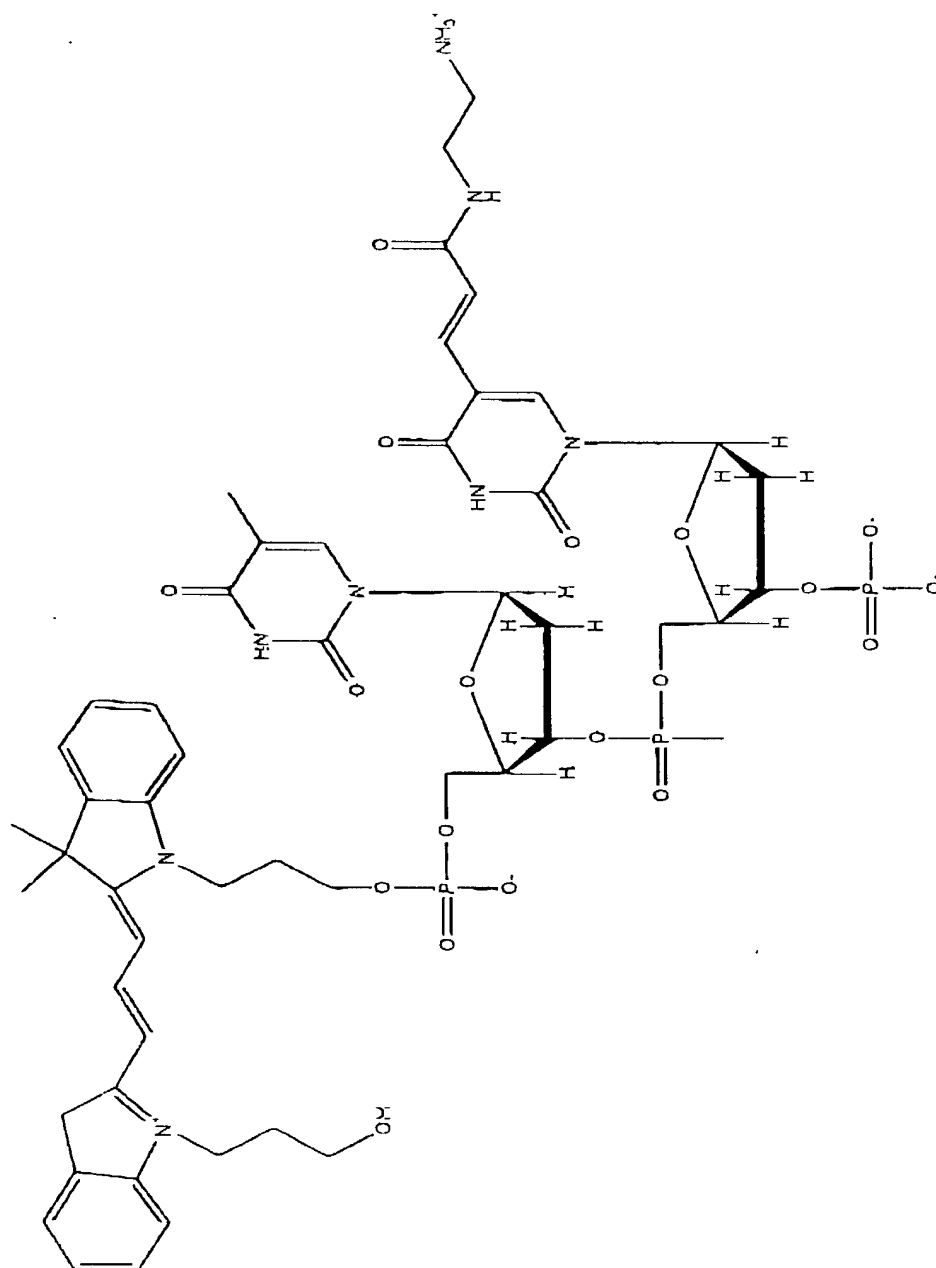


FIGURE 57



57

69

FIGURE 58

76

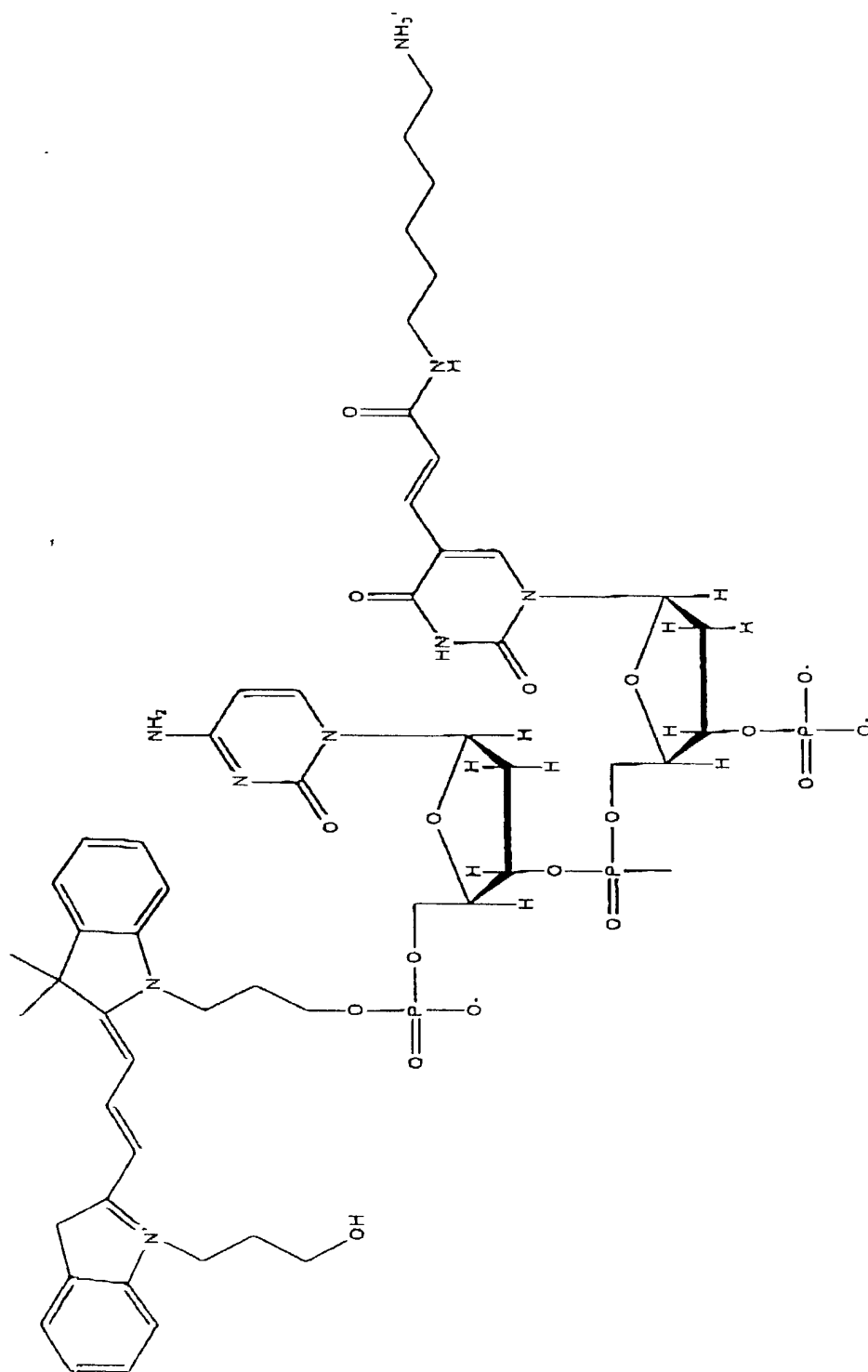
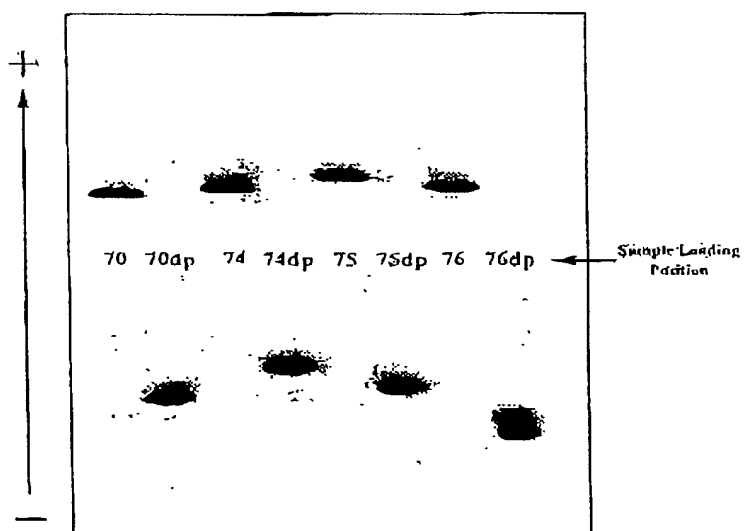


FIGURE 59



71

FIGURE 60

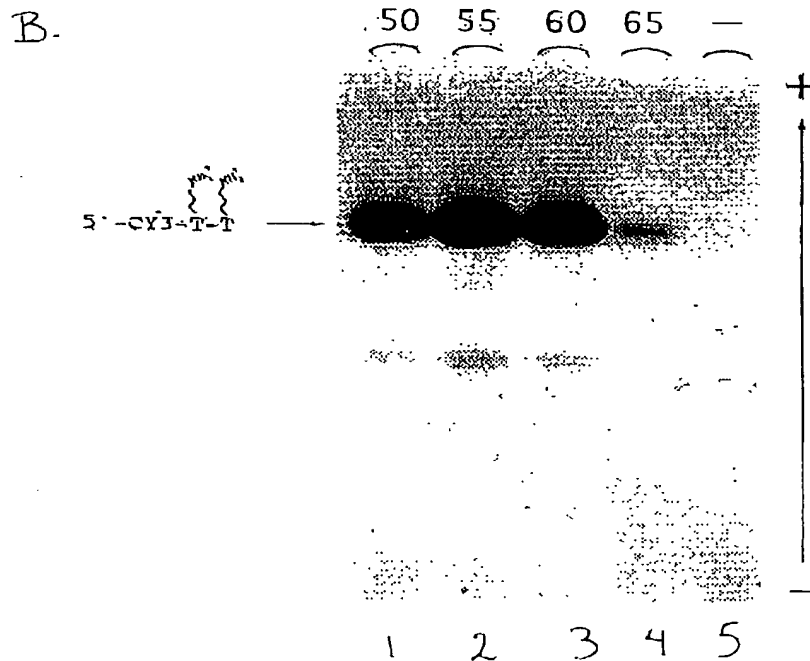
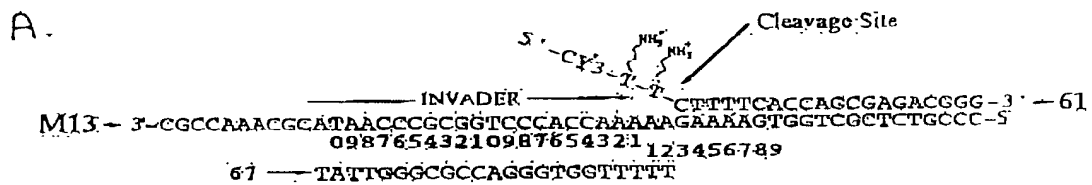


FIGURE 62

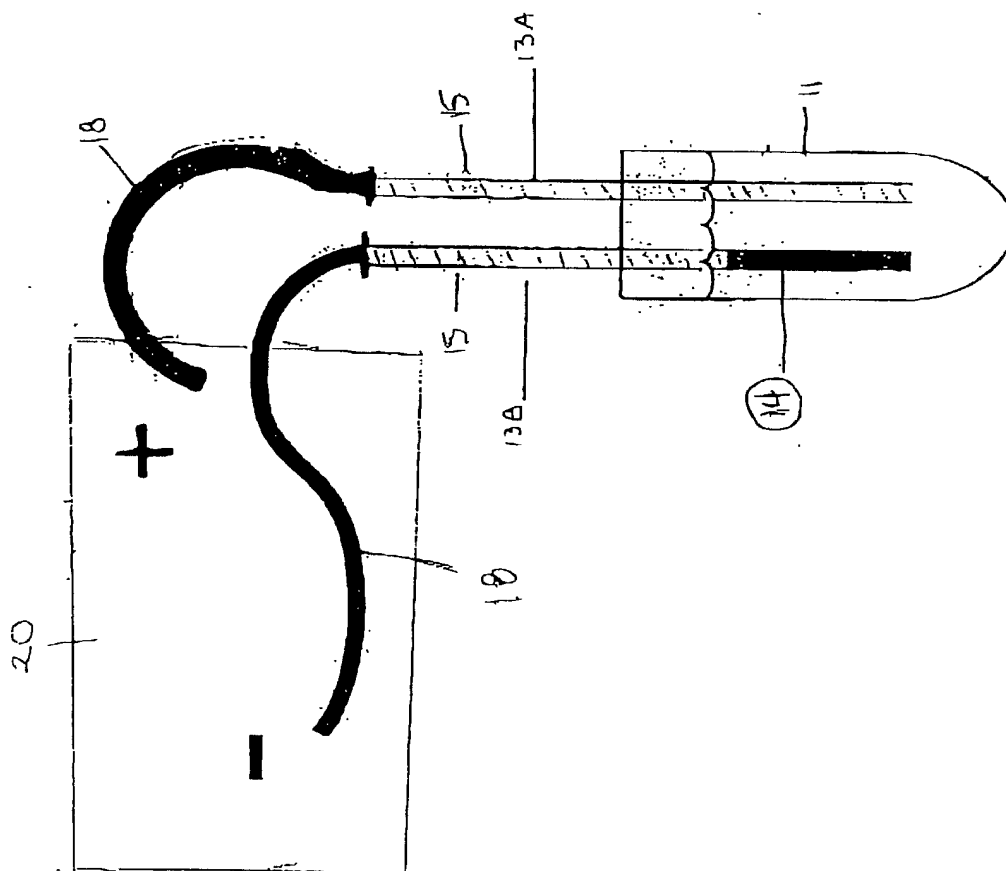


FIGURE 63

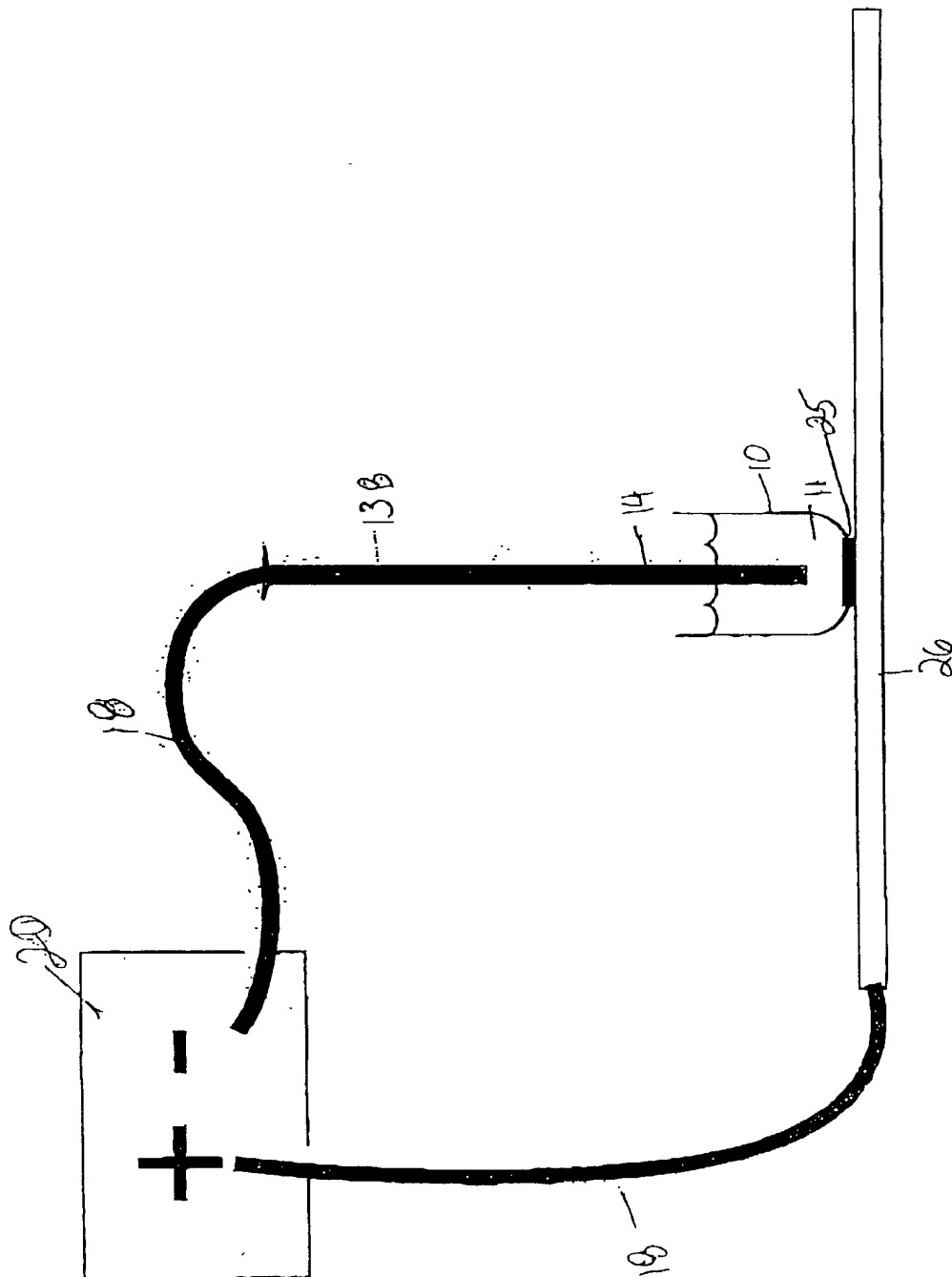


FIGURE 64

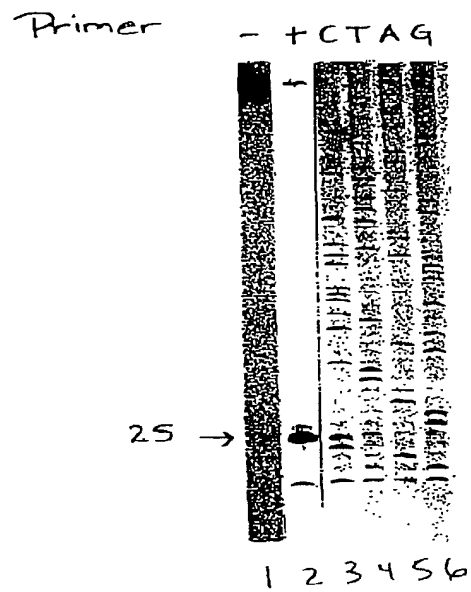


FIGURE 65

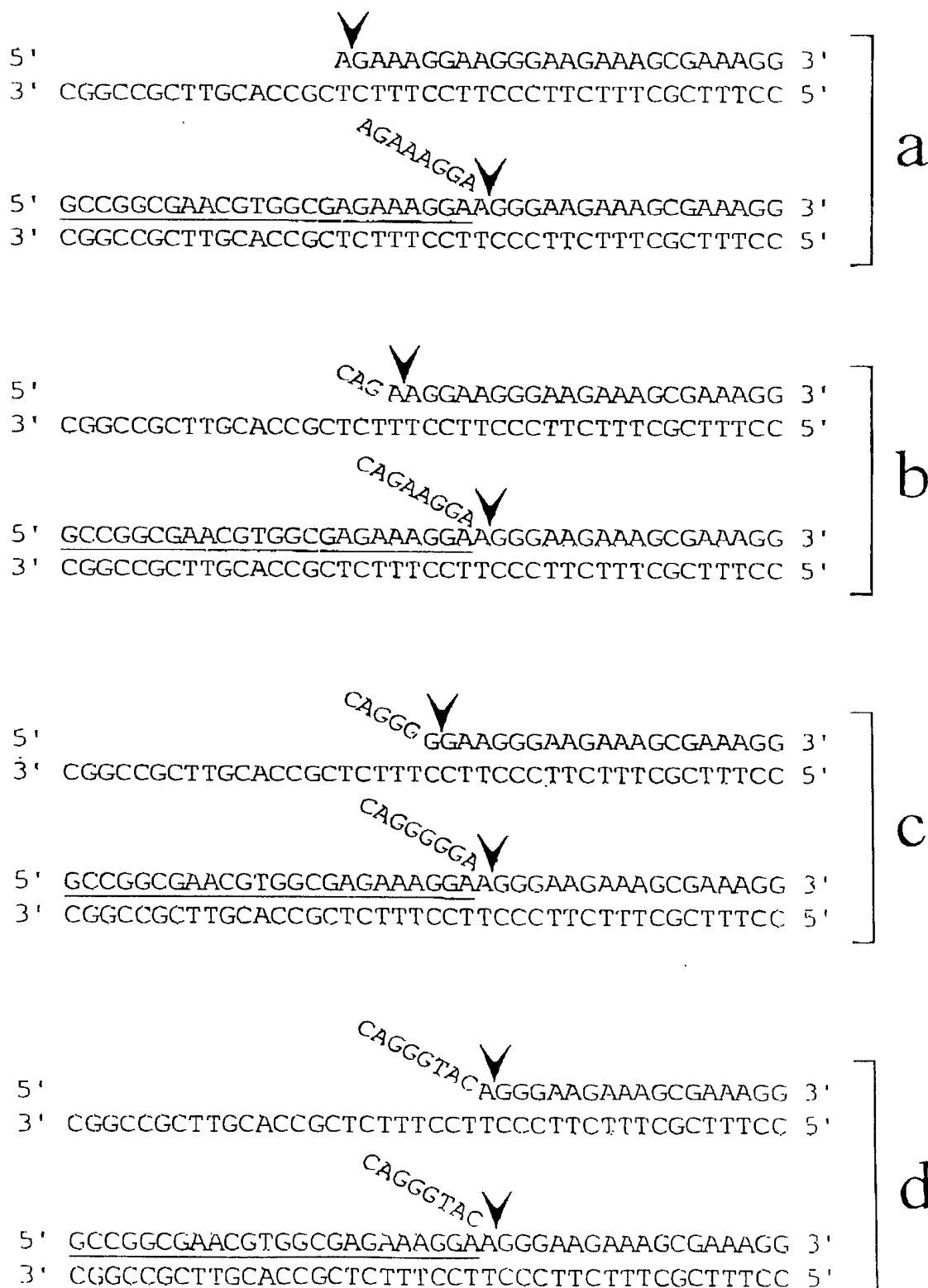


FIGURE 66

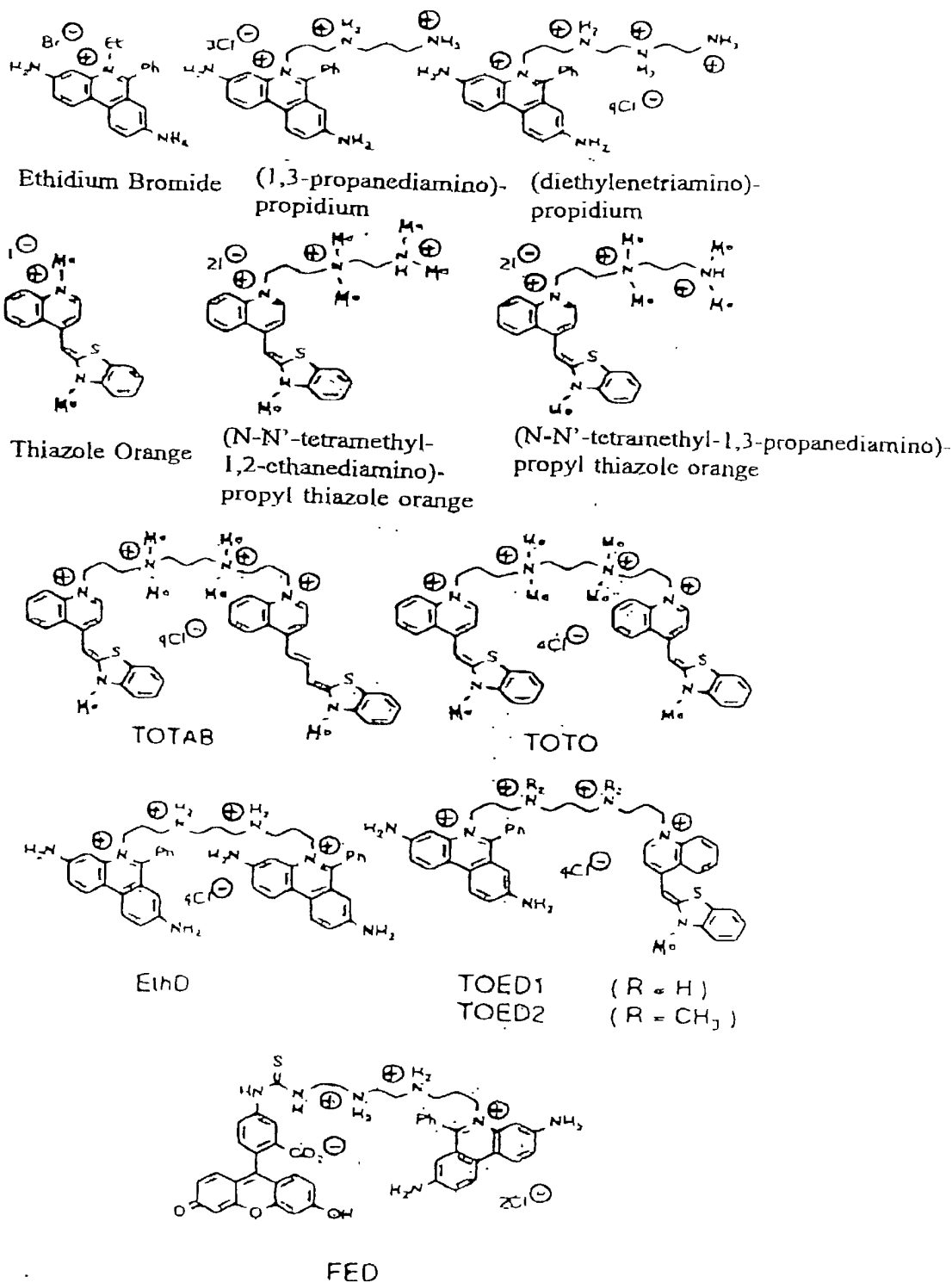


FIGURE 67

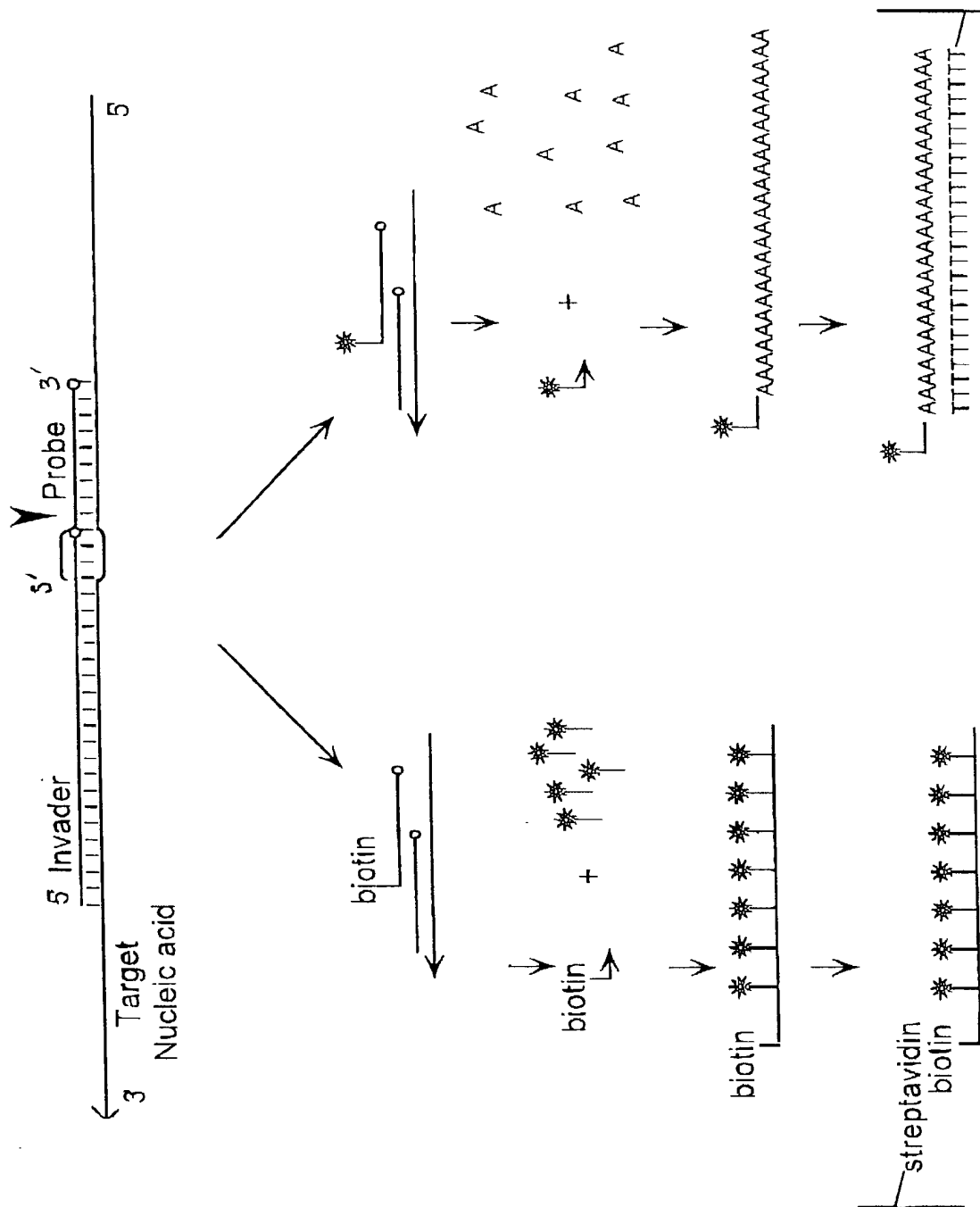


FIGURE 68

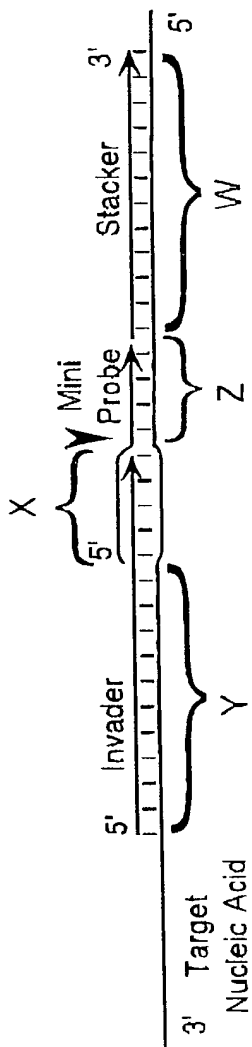


FIGURE 69



FIGURE 70-B

	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQAASYMAKKGDVWVVSDDYDALLYGAPRVVRNLTTTKEM----	MJAFEN1.PRO					
130	MLJEDAKKLLLELMGIPIVOAPSEGEAQAAYMAAKGSVYASASDDYDSLLFGAPRLVRNLTTGKRKLPGK	PFUFEN1.PRO					
136	QHNOECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ	HUMFEN1.PRO					
134	QHNOECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ	MUSFEN1.PRO					
134	EHNEEAQKLLGLMGIPYIIAPTEAEAOCAELAKKGKVYAAASEDMOTLCYRTPFLLRHLTFSEAKKEPIH	YST510.PRO					
131	OMIKEVOELLSRFGIPYITAPMEAEAOCAELLQNLVDGIIITDQSOVFLFGGTKIYKNMFHEKNY----	YSTRAD2.PRO					
131	YMIKECOELLRLFGLPIYIVAPQEAEAGCSKLELKLVDGIVTDQSDVFLFGGTRVYRNMFNONKF----	SPORAD13.PRO					
131	OMFLESOELLRLFGLPIYIOAPMEAEAOCAILDLTQTSGTITDQSDIWLFGARHVVYRNFNKNKF----	HUMXPG.PRO					
131	OMFLESOELLRLFGLPIYIOAPMEAEAOCAVLDLSDQTSGTITDQSDIWLFGARHVVYKKNFKNKF----	MUSXPG.PRO					
131	OMCLESOELLQLFGIPYIVAPMEAEAOCAILDLTQTSGTITDQSDIWLFGARHVVYKNFFSQNKH----	XENXPG.PRO					
111	DHVVYKTNALLTELGIKVIJAPGOGEAOCARLEDLGVTSGCITTDQFYFLFGGKNLYRFDFTAGT-----	CELRAD2.PRO					

	220	230	240	250	260	270	280
195	-----	P E L I E N E V L E D L R I S L O D L I D I A I F M G T D Y N P G V	--K--	G I G F K R A Y E L V R S G V A K	--D V		M J A F E N 1 . P R O
196		N V Y V E - I K P E L I L E E V L K E L K L T R E K L I E L A I L V G T D Y N P G G I	--K--	G I G L K K A L E I V R H S K D P L A K F			P F U F E N 1 . P R O
197		E F H L S R I L O E L G L N O E Q F V O L C I L L G S D Y C E S I R G I G P K R A V D L I O K	--H K S I E E I V R R L O P N	-----K Y			H U M F E N 1 . P R O
198		E F H L S R V L O E L G L N O E Q F V O L C I L L G S D Y C E S I R G I G A K R A V D L I O K	--H K S I E E I V R R L O P S	-----K Y			M U S F E N 1 . P R O
199		E I D T E L V L R G L O L T I E Q F V O L C I M L G C D Y C E S I R G V G P V T A L K I J K T	--H G S I E K I V E F I E S G E S N N T K W				Y S T 5 1 0 . P R O
200		F Y D A E S I L K L G L D R K N M I E L A Q L L G S D Y T N G L K G M C P V S S I E V J A E F	--G N L K N F K D W Y N N G O F O K R K				Y S T R A O 2 . P R O
201		L Y L M O D M K R E F N V N O M D L I K L A H L L G S D Y T M G L S R V G P V L A L E I L H E F P G D T G L F E F K K W F O R L S T G H A S					S P O R A D 1 3 . P R O
202		Y Y G Y V D F H N O L G L D R N K L I N L A Y L L G S D Y T E G I P T V G C V T A M E I L N E F P G H G L E P L L K F S E W W H E A Q K N P					H U M X P G . P R O
203		Y Y Q Y V D F Y S O L G L D R N K L I N L A Y L L G S D Y T E G I P T V G C V T A M E I L N E F P G R G L D P L L K F S E W W H E A Q N N K					M U S X P G . P R O
204		Y Y Q Y A D I F H N O L G L D R S K L I N L A Y L L G S D Y T E G I P T V G Y V S A M E I L N E F P G O G L E P L V K F K E W W S E A O K D K					X E N X P G . P R O
205	-----	-----	-----	S S T A C L H D I M H L S L G R M F M	-----		C E L R A O 2 . P R O

FIGURE 70-C

	290	300	310	320	330	340	350	
251	LKKEVEYYDEIKRIFKEPKV	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
265	QKOSDVOLYAIKEFFLNPPV	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
269	PVPENWLHKEAHQLFLEPEV	-----	-----	-----	-----	-----	-----	HUMFEN1.PRO
267	PVPENWLHKEAQOLFLEPEV	-----	-----	-----	-----	-----	-----	MUSFEN1.PRO
272	KIPEDWPYKQARMLFLDPEV	-----	-----	-----	-----	-----	-----	YST510.PRO
265	QETENKFEKDLRKKLVNNEI	ILODDFPSVMVYDAYMRPEVD	HTTPTFVVGVPOLDMLRSF	MKTOLGWPHE				YSTRAD2.PRO
268	KNDVNTPVKKRINKLVGK-	ILPSEFPNPLVDEAYLHPAV	DDSKOSFOWGIPOLOEL	RQFLMATVGSW	KQ			SPORAD13.PRO
268	KIRPNPHDTKYKKKL	--RTLOLTPGFPNPAVAE	AYLKPVVQDSKGSFLWGK	POLCKIREFCQR	YFGWNR			HUMXPG.PRO
268	KVAENPYDTKYKKKL	--RKLOLTPGFPNPAVAD	AYLRPVVDDSRGSFLWGK	PDVOKIREFCQR	YFGWNR			MUSXPG.PRO
268	KMRPNPNDTKYKKKL	--RLDLQOSFPNPAVAS	AYLKPVVDESKSAFSWGR	POLCKIREFCES	RFGWYRL			XENXPG.PRO
194	-----EKKVSRPHLJ	STALLGCOYFORGVQNI	GVSVD-ILGEFGDDG	NEEIDPHVILDRF	ASYVRE			CELRAD2.PRO

	360	370	380	390	400	410	420
3300	RVKHHVDKLYNLIA	-----	-----	-----	-----	-----	MJAFEN1.PRO
3314	RVKNGLERLKKA	-----	-----	-----	-----	-----	PFUFEN1.PRO
3320	RIRSGVKRLSKSRQGS	-TQRLDOFFKVT	-----	-----	-----	-----	HUMFEN1.PRO
3318	RIRSGVKRLSKSRQGS	-TQRLDOFFKVT	-----	-----	-----	-----	MUSFEN1.PRO
3323	RVKSGISRLKKGLKSG	-JQRLDGFFQVV	-----	-----	-----	-----	YST510.PRO
3335	KSDEILPLIRDVNRKK	-----	-----	-----	-----	-----	YSTRAD2.PRO
3337	RTNEVLLPVIQDMHKKQF	-----	-----	-----	-----	-----	SPORAD13.PRO
3336	KTDESIFPVLKQLDAQ	TOLRIDSFFRLAQQEKEDAKRIKSQRLNRAVTCMLRKEKEAASE	IEAVSVAM	-----	-----	-----	HUMXPG.PRO
3336	KTDESILYPLKHLNAH	OTQLRIDSFFRLAQQEKQDAKL(KSHRLSRVATCMLRKEREKAPELTKVTEAM	-----	-----	-----	-----	MUSXPG.PRO
3336	KTDEVLLPVLKOLNAO	TOLRIDSFFRLQHEAAG	---LKSORLRRAVTCMKRKERDVEAEVEAAVAVM	-----	-----	-----	XENXPG.PRO
257	EIPARSED	TORKLRLRRKKYNFPVGFPCNDVHNA	ITMYLRPPVSSEIPKI	IPR	----	----	CELRAD2.PRO

FIGURE 70-D

[illegible]

	500	510	520	530	540	550	560	
314	-----	-----	-----	-----	-----	-----	MJAFEN1 PRO	
327	-----	-----	-----	-----	-----	-----	PFUFEN1 PRO	
352	SAKRKEPEPKGT-----	-----	-----	-----	-----	-----	HUMFEN1 PRO	
350	SAKRKEPEPKGPA-----	-----	-----	-----	-----	-----	MUSFEN1 PRO	
354	KEGLAAAKRAOE-----	-----	-----	-----	-----	-----	YST510 PRO	
364	-----	-----	PREYISGDKKLN	TSKRISTATGKL	-----	-----	YSTRAD2 PRO	
429	RRKMMASKNSSDSC	SDSEDNFLASL	TPKTNSSSIS	LENLPRKTL	STSL	-----	SPORAD13 PRO	
476	NVORRTAAKEPKT	SASDSONSVKEAP	VKNGGATTSS	SSDDGGKEK	MVLVTAR	SVFGKKRRKLR	RARG HUMXPG PRO	
469	SARQSAEAESSK	IGCSOVPOLVRO	SPHGRQGC	VSSTSSDSE	EDGEOKAK	TVLVTAR	PVFGKKRRKLR	KSMK - MUSXPG PRO
458	-----	GSSDAEDLP	SGLIDKOSQ	SVIGROKAS	NKVESSSSD	DOEDRTVM	TAKPVFGKKT	SKTMKE XENXPG PRO
387	WMRK8KRSE	SP01LOHHAK	RQVPORK	-----	-----	-----	RSVKIRAFKPYPTOV	J CELRAD2 PRO

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FIGURE 71

